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Thanks Prema Mertz, Ph.D. Art Unit 1646
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9YMP5 PRELIMINARY; PRT; 778	1 9YMP5 PRELIMINARY; PRT; 778 9YMP5.
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782 1534 1627 304 826 506 865 270 708

Q28298 Q962Q0 L Q91YT3 3 Q9YHD5 Q9NWY9 Q9NWY9 3 Q98SN6 P79391 4 Q9YHD7

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Q91yt3 mus musculu Q9yhd5 rana catesb

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Best Local
            EMBL; APO
Flagella;
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MEDLINE-20512502; PubMed-11058132;
Takami H., Nakasone K., Takaki Y.,
Takami F., Hirama C., Nakamura Y., Og
                                 "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis Nucleic Acids Res. 28:4317-4331(2000).

EMBL; AP001515; BAB06166.1; -.
                                                                                                                                                                                                                                                                                                           Bacillus/Staphylococcus
NCBI_TaxID=86665;
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Bacteria; Firmicutes; Bacillus/Clostridium
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01-JUN-2001
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EMBL; AP001519; BAB07319.1;
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01-OCT-2000
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Fuji F., Hirama C.,
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NCBI_TaxID=86665;
                                                                                                                                Horikoshi K.;
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MEDLINE=20512582; PubMed=11058132;
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(TIEMBLrel. 15, Last sequence update)
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ROTEIN REQUIRED FOR FLAGELLAR FORMATION.
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Nakamura Y., O
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, Ogasawara
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                                                                                                                                                , Sasaki R., ma.
""hara S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20014706; PubMed=10545595;
Oka A., Tamiya G., Tomizawa M., Ota M., Katsuyama Y., I
Shiina T., Yoshitome M., Lizuka M., Sasao Y., Iwashita
Kawakubo Y., Sugai J., Ozawa A., Ohkido M., Kimura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                  LQLELSRAQEARRWW--
                                                                                                                                                                                               LSVRIA----DKKYYPSSQDSSSAAAPQLLIVLLGLSA 177
                                                                                                                                                                                                                               LMVQLKAQELEHSDSVKQLKGQVASLQEKVTSQSQEQAILQRSLQDKAAEVEVERMGAKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 86118 MW;
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Pred. No. 0.
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Pred. No. 1.4;
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Catarrhini;
                                                                                 PRT;
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i; Hominidae; Homo.
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Best Local S
Matches 39
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01-NOV-1999
01-DEC-2001
                                                                                      Shiina S., Tamiya G., Oka A., Inoko H.;
"Homo sapiens 2,229,817bp genomic DNA of 6p21.
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ
EMBL; AB003943; BAA82158.1;
EMBL; AP000509; BAB63313.1;
SEQUENCE 756 AA; 85951 MW; 3D109AF0EEEAB9F
                                                                                                                                                                                                                                           Oka A., Tamiya G., Makino S., Tomizawa M., Yar
Watanabe K., Yamazaki M., Tashiro H., Kimura k
"HCR-a helix coiled-coil rod homologue."
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asumalahti K., Laitinen T., Itkonen-Vatjus R., Lokki M.-L., Suomela S., Snellman E., Saarialho-Kere U., Kere J.; "A candidate gene for psoriasis near HLA-C, HCR (PgB), is highly polymorphic with a disease-associated susceptibility allele."; Hum. Mol. Genet. 9:1533-1542(2000).

EMBL; AF216493; AAF74221.1; -. SEQUENCE 756 AA; 86058 MW; 8E4D03358B62DEB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                            Submitted
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                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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  RDGLRAVME - - -
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                          40;
                                      Similarity
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(TrembLrel. 12, Last sequence update)
(TrembLrel. 19, Last annotation updat
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 -CRNVTHLL----QQELTEAQKGFQDVEAQ-AATC-----
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24.7%;
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EMBL/GenBank/DDBJ
                          Score 104.5;
Pred. No. 1.4;
32; Mismatches
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Pred. No. 1.4;
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  -NHTVMA
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Best Local
SEQUENCE FROM N.A.
TISSUE-COLON MUCOSA;
Watanabe K., Kumagai A., Itakura S., Y.
Suzuki Y., Obayashi M., Nishi T., Shib
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
"NEDO human rFEB-2000) to the EMBL/GenBa
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Q9NXK3;
Q1-OCT-2000
Q1-OCT-2000
Q1-OCT-2000
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"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ EMBL; AK00204; BAA91007.1;
SEQUENCE 782 AA; 88616 MW; F472FE544F627CE
                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
CDNA FLJ20210 FIS, CLONE COLF1787.
Homo sapiens (Human).
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TISSUE=COLON MUCOSA;
Watanabe K., Kumagai
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                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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01-OCT-2000
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Mammalia; Eutheria;
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Pred. No. 1.7;
32; Mismatches
      project.";
EMBL/GenBank/DDBJ
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                                                        Ψ.,
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RESULT Q28298 ID 992 ID
       RESULT Q962Q0 ID 999 AC Q99 Q90 O1. DT 01. DE ALL OC GUE OC GUE OC GUE OC GUE OC RN NCI RN SEE RA ELL
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Best Local S
Matches 26
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Best Local
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Q28298;
O1-NOV-1996 (TrEMB)
O1-NOV-1996 (TrEMB)
O1-DEC-2001 (TrEMB)
RIBOSOME RECEPTOR
P180.
                                                                                                                                                                                                                                             Q962Q0;
                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TREMBLRel. 19, Last sequence up
01-DEC-2001 (TREMBLREL 19, Last annotation
AXONEMB-ASSOCIATED PROTEIN GASP-180.
Giardia lamblia (Giardia intestinalis).
Giardia lamblia (Giardia intestinalis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Cranidae; Canidae;
    SEQUENCE FROM N. Elmendorf H.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-95310363; PubMed-7790375;
Wanker E.E., Sun Y., Savitz A.J., Meyer D.I.;
"Functional charcterization of the 180 kDa ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora; 
NCBI_TaxID=9615;
                                                                              NCBI_TaxID=5741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Cell Biol. 130:29-39(1995).
EMBL; X87224; CAA60676.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                         907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      847
                                                                                                                                                                                                                                                                                                                                                                                                                                  115 ELEGEITTLNHKLQDA-SAEVERLRRENQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 RDSLHATAELLQVRVQSLTHILALQEEELTRKVQPSDSLEPEFTRKCQSLLNRWREKVFA
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                                                                                                                                                                                                                                                                                                                                                                                 QLQGKIRTLQEQLENGPNTQLARLQQENSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LMASLDAEKAQGQKKVEELEGEITTLNHK-------LQDASAEVERLRENQV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAAVAKSKLREVNKELAAEKAKAAAGEAKVKKQLVAREQEITAVQARIEASYREHVKEVQ 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSVRI-----ADKKYYPSSQDSSSAAAPQLLIVLLGLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQLELSRAQEARROW----QQQTASAEEQLRLVVNAVSS 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LMVQLKAQELEHSDSVKQLKGQVASLQEKVTSQSQEQAILQRSLQDKAAEVEVERMGAKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 01,
(TrEMBLrel. 01,
(TrEMBLrel. 19,
                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
       Rohrer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 102.5; [Pred. No. 4.5; 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 103.5; D
Pred. No. 1.7;
32; Mismatches
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Last sequence up
Last annotation
       La
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Vigne
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                                                                                                                                                                                                                                                                      1627
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    E.A.,
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                                                                                                                                                                    on update)
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       Nash
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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[7]
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RESULT
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AC Q5
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Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                  Q9YHD5;
01-MAY-1999
01-MAY-1999
01-DEC-2001
                                                                         MYOSIN
MHC-4.
    Amphibia;
                          Eukaryota;
                                                 Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                 Q9YHD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (OCT-2001) to the
EMBL; BC014811; AAH14811.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MACROPHAGE GALACTOSE N-ACETYL-GALACTOSAMINE SPECI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1401
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF400249; AAF81740.1; -.
SEQUENCE 1627 AA; 179270 MW; 021EED9763907DCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q91YT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1284 LRESAEALQDKLHALSDSRAADGDLQKLVEQLEKDLSGAKELVAERDATIDELKQRLRDT 1343
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                                                                                                                                                                                                                                                                                                                                144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 36; Conserv
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DHVQQLRKDLKALTCQLANLK--
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                                                                                                                                                                                                                                                                                                                                                                         AEVERLRRENQVLSVRIADKKYYPSSQDSSSAAAP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDVEAQAATCNHTVMALMASLDAEKAQGQ-----KKVEELEGEI----TTLNHKLQDAS
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                                                                                          7-1999 (TremBLrel. 1
7-1999 (TremBLrel. 1
3-2001 (TremBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1402
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    Batrachia;
                            Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                 (FRAGMENT).
                          Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34622 MW;
    Anura;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.5%;
27.9%;
                                                                                                             10, Created)
10, Last sequence update)
19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
    Neobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 101.5; D
Pred. No. 0.86;
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Pred. No. 4.8;
                          Craniata;
                                                                                                                                                                                                                                                                                                                                -NNGSEVACCP
                                                                                                                                                                                                                 PRT;
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  Vertebrata;
a; Ranoidea;
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SPECIFIC
                                                                                                                      update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -LEAQPTATTVYPESGEEVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60;
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  Euteleostomi;
Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5,
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Best Local S
Matches 36
                                                                                                                                                   Matches
                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                               Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashii Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka Tanaka T., Vasahura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. SEMBL, AKOO533; BAA91236.1;
SEQUENCE 506 AA; 57358 MW; B41ABD7DB1EFA495 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          Q9NWY9;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                  CDNA FLJ20526 FIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 YWY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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EMBL; AF097907; AAD13772.1; -.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR000533; Tropomyosin.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hu H., Merrifield P., Atkinson B.G.; 
"Expression of the Myosin Heavy Chain Genes 
Thyroid Hormone-induced Metamorphosing Rana
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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TISSUE-TAIL MUSCLE, HINDLIMB MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 KANSEACR-----DGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 36; Conserv
                                                 8
                                                                        86
                                                                                                                       54 RDGLRAVME-----CRNVTHLL---QQELTEAQKGFQDVEAQ-AATC-----NHTVMA
                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KMKNAYEEALEQVETLKRENKNLQQEISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLNHKLQDASAEVERLRRENQVLSVRIAD
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LQLELSRAQEARRRWQQQTAS-AEEQLRLVVNAVSS
                      QVLSVRIADKKYYPSSQDSSSAAAPQLLIVLLGLSA
                                              LMVQLKAQELEHSDSVKQLKGQVASLQEKVTSQSQEQAILQRSLQDKAAEVGVERMGAKG
                                                                       LMASLDAEKAQGQKKVEELEGEITTLNHK------LQDASAE--VERLRREN 141
                                                                                                RDSLHATAELLQVRVQSLTHILALQEEELTRKVQPSDSLEPEFTRKCQSLLNRWREKVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                826 AA;
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                                                                                                                                                                                                                                                                                                                                                         Chordata;
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                                                                                                                                                              11.3%;
26.3%;
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                                                                                                                                                                                                                                                                                                                                                                                  KAT10627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Pred.
                                                                                                                                                              Score 100.5;
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8F9E3B0579D0F483 CRC64;
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No. 2.7
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162
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                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---- AEKAQGQKKVEELEGEIT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the Tail Muscle of catesbeiana Tadpoles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
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                                                                                                                                                                                                                                                                              Tashiro H.,
anaka T.,
                                                                                                                                                 Indels
                                                                                                                                                                          Length
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RESULT P79391 P79391 P7 AC P7 OI DT OI DT OI DT OI DE LE OC EU OC Ma
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Best Local S
Matches 33
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NON_TER
SEQUENCE
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RHO-ASSOCIATED COILED-COIL FORMING KINASE 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wei L., Roberts W., Wang L., Yamada M., Zhang
Rivkees S.A., Schwartz R.J., Imanaka-Yoshida K
"Rho kinases play an obligatory role in verteb
organogenesis.";
                                                                 P79391:
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
LECTIN-LIKE OXIDIZED LDL RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00109; TYRKINASE.
SMART; SM00074; HR1; 1.
SMART; SM000220; S_TKC; 1.
SMART; SM00133; S_TK_X; 1.
SMART; SM00219; TYrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2001) to the EMBL/GenBank/DDBJ-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY EMBL; AF347075; AAK29627.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAD-ROSCALIA (Chicken).

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Calliformes; Phasianidae; Phasiani
Bos taurus (Bovine).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                             P79391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00107; PROTEIN_KINASE_ATP; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pram;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding; Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                 842
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                                                                                                                                                                                                                                                                                                                                                              150 DKKYYPSSQDSSSAAA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93
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                                                                                                                                                                                                                                                                                                                 EEQYFELSQESKKAAS
                                                                                                                                                                                                                                                                                                                                                                                                                 KTQVKELKEEIDEKNKETQRKMQELQNEKETLTTQLDLAETKAESEQLAR-----ALL
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IPR000961; Pkinase_C.
IPR000861; REM_repeat.
IPR002290; Ser_thr_pkinase
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865 /
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                                                                                                                                                                                             PRELIMINARY;
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101138
Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.2%;
24.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 100; DB Pred. No. 3.8; 30; Mismatches
                                                                                                                                                                                             PRT;
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OF PROTEIN KINASES
  Pecora; Bovoidea
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Best Local Similarity 25.9%; Pred. No. 1.1;
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SEQUENCE FROM N.A.

MEDLINE=97205278; PubMed=9052782;

Sawamura T., Kune N., Aoyama T., Moriwaki H., Hoshikawa H., Aiba Y.,

Tanaka T., Miwa S., Katsura Y., Kita T., Masaki T.;

"An endothelial receptor for oxidized low-density lipoprotein.";

Nature 386:73-77(1997).

EMBL; D89049; BAA19005:1; -.

EMBL; D89049; BAA19005:1; -.

HSSP; P20693; HLJ.

InterPro; IPR001304; lectin_c.

Pfam; PF00059; lectin_c: 1.

SMART; SM00034; CLECT; 1.

PROSITE; P550041; C_TYPE_LECTIN_2; 1.
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DOMAIN CARBOHYD CARBOHYD This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial Ishikawa J., Kaisho T., Tomizawa H., Lee B.O., Kobune Y., Inazawa J., Oritani K., Itoh M., Ochi T., Ishihara K., Hirano T.; "Molecular cloning and chromosomal mapping of a bone marrow stromal cell surface gene, BST2, that may be involved in pre-B-cell growth."; Genomics 26:527-534(1995). entities requires a license agreement (S or send an email to license@isb-sib.ch). Eukaryota; Metazoa; Mammalia; Eutheria; SEQUENCE Transmembrane; MIM: EMBL; D28137; BAA05679.1; MEDLINE=95331788; PubMed=7607676; NCBI\_TaxID=9606; TRANSMEM DOMAIN FUNCTION: MAY BE INVOLVED IN PRE-B-CELL GROWTH.
SUBCELLULAR LOCATION: Type II membrane protein.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LIVER, AND BRAIN.

DISEASE: MAY PLAY A ROLE IN B-CELL ACTIVATION IN RHEUMATOID ARTHRITIS (RA). AND PLACENTA. LOWER LEVELS IN PANCREAS, KIDNEY, SKELETAL MUSCLE 600534; -180 21 49 65 92 Glycoprotein; 180 180 65 92 Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo. 19769 100.0%; ¥¥, Signal-anchor: Polymorphism.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL). N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
V -> F (IN DBSNP:1804402). V -> F (IN DBSNP:1804402). /FTId=VAR\_012067. CAF52340D69061EE CRC64; Score 889; DB 1; Pred. No. 1.3e-63; ; Mismatches 0; noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/ Length 180; LUNG,

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-I- FUNCTION: RECEPTOR WITH AN AFFINITY FOR GALACTOSE AND COULD BE INVOLVED IN ENDOCYTOSIS.

-I- SUBCELLULAR LOCATION: Type II membrane protein.

-I- TISSUE SPECIFICITY: KUPFFFER CELLS.

-I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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SMART; SM00034; CLECT; 1.
SMART; SM00503; SynN; 1.
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"Structure of the gene for a carbohydrate-binding rat Kupffer cells.";
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"Molecular cloning and sequencing of a cDNA for inding receptor unique to rat Kupffer cells."
J. Biol. Chem. 263:7487-7492(1988).
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A38674; A38674.
; P20693; 1HLJ.
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(POTENTIAL).

EXTRACELLULAR (C-TYPE LECTIN (BY SIMILARITY.BY SIMILARITY.BY SIMILARITY.
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SIGNAL-ANCHOR
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Sciurognathi; Muridae; Murinae; Rat
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OR (TYPE-II
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RESULT 3
K1CR_MOUSE
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Best Local
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01-NOV-1988 (Rel. 09, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
                                     SEQUENCE OF 1-131 FKUM N....
SEQUENCE OF 1-131 FKUM N....
MEDLINE-88255838; PubMed-2454868;
MShima R.G., Trevor K., Shevinsky L.H., Ryder O.A., Cecena G.;
"Tdentification of the gene coding for the Endo B murine cytokeratin
"Tdentification of the gene coding for the Endo B murine cytokeratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=86085876; PubMed=2416755;
MEDLINE=86085876; PubMed=2416755;
                                                                                                                                                        Singer P.A., Trevor K., Oshima R.G.;
"Molecular cloning and characterization
expressed in preimplantation mouse embry
                                                                                                                                                                                                                                                                                      TISSUE=Teratocarcinoma;
Alonso A., Weber T., Jorcano J.L.;
"Cloning and characterization of keratin D,
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-89196920; PubMed-2467843;
Ichinose Y., Morita T., Zhang F.,
                                                                                                                                                                                                                                                           cytoskeletal protein induced during
teratocarcinoma cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keratin, type I cytoskeletal 18 (Keratin D).
                               Genes Dev. 2:505-516(1988).
                                                                                                                                                                                                                                              Roux's Arch. Dev. Biol. 196:16-21(1987)
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             Gene 70:85-95(1988).
                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRT18 OR KRT1-18 OR
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Nozaki M., Matsı
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Sciurognathi; Muridae;
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  TWO TYPE
KERATIN 8
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o differentiation of
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Best Local S
Matches 51
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EMBL; M36376; AAA393973.1; -.
EMBL; M1686; AAA3939011; -.
EMBL; W10217; CAA66365.1; -.
PIR; A25621; A25621.
PIR; A26428; A28428.
PIR; JT0406; JT0406.
SWISS-2DPAGE; P05784; MOUSE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:96692; Krt1-18.
InterPro; IPR001664; IF
InterPro; IPR00257; Keratin_I.
Pfam; PF00038; filament; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The European Bioinformatics Institute of Hioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on if the by non-nonfit institute.
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                                                                                                                   GLSALL
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                                                                                                                                                          TKSAEIRDAETTLTELRRTLQTLEIDLDSMKNQNINLENSLGDVEARYKAQMEQLNGVLL
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27.4%;
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O-LINKED (GLCNAC) (IO-LINKED (GLCNAC) (IO-LINKED (GLCNAC) (IO-LINKED (IN REF. 2))

D -> N (IN REF. 2)

A -> G (IN REF. 2)
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STUTTER.
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LINKER 1.
COIL 1B.
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Pred. No. 0.
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ACETYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINKER 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4D5B0E9C7732F2F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                             .51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY
(BY)
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y SIMILARITY).
Y SIMILARITY).
Y SIMILARITY).
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24

LGIGILVLLIIVILGVPLIIFTIKANSEACRD--GLRAVMECRNVTHLLQQELTEAQKGF

Query Match Best Local S Matches 36

Similarity

11.2%;

Conservative

37;

Score 99.5; D Pred. No. 0.47 37; Mismatches

DB .47;

Length 304; Indels

49; 1;

33;

Gaps 81

7;

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DOMAIN
DOMAIN
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
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Ol-FEB-1996 (Rel. 33, Last sequence update)
Ol-NOV-1997 (Rel. 35, Last annotation update)
Macrophage asialoglycoprotein-binding protein (M-ASGP-BP) (Macrophage galactose/N-acetylgalactosamine-specific lectin) (MMGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MMGL_MOUSE
P49300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Purification and characterization of a lectin-like molecule specific for galactose/N-acetyl-galactosemine from tumoricidal macrophages."; J. Biochem. 104:600-605(1988).
-i- FUNCTION: RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92268032; PubMed=1587794;
Sato M., Kawakamyi K., Osawa T., Toyoshima S.;
"Molecular cloning and expression of cDNA enco-
acetylgalactosamine-specific lectin on mouse t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----
                                                                                                                                                                                                                                              PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Glycoprotein; Transmembrane; Calcium; Signal-anchor.
Lectin; Glycoprotein; Transmembrane; CPTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; S36676; AAB22171.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -: SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oda s.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89197865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C3H/HEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 102-120 AND 137-151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        macrophages."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C3H/HEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                   SMART; SM00034; CLECT;
                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00059; lectin_c;
                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:96975; Mgl.
InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                               FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Biochem. 111:331-336(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMO-OLIGOMER.
SUBCELLULAR LOCATION: Type II men
TISSUE SPECIFICITY: IS EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: RECOGNIZES TERMINAL UNITS. MAY PARTICIPATE IN THE MACROPHAGES AND TUMOR CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MACROPHAGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                    P06734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sato M.,
          304 AA;
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172
173
201
274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toyoshima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=3241002;
                                                       304
298
184
296
288
74
          34596
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          W.
SIGNAL-ANCHOR (TYPE-II MEMBRANE PR
(POTENTIAL).
EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Osawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane protein.
SED ON THE SURFACE OF ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALACTOSE AND N-ACETYLGALACTOSAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              f cDNA encoding on mouse tumori
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tumoricidal
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                              .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUMORICIDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL
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  Query Match
Best Local Similarity
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                                                                                 MOD_RES
MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         060763;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2011 (Rel. 40, Last annotation update)
General vesicular transport factor pl15 (Transcytosis associated protein) (TAP) (Vesicle docking protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWI
                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as not removed modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98148093; PubMed=9478999; Sohda M., Misumi Y., Yano A., Takami N., The docking of the vesicle docking association with the Golgi membrane.";
                                                                                                                                                                       DOMAIN
                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                  MIN,
                                                                                                                                                                                                                                                                                                                   EMBL; D86326;
                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                    DOMAIN
                                                                                                                                                                                                              Phosphorylation.
                                                                                                                                                                                                                                    Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION PROMOSTES DISSOCIATION.
SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DHVQQLRKDLKALTCQLANLK----NNGSEVACCP
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                                                                                                                                                                                                                                                                      IPR000225; Armadillo.
                                                                                                                                                                                                                               Protein
                                                                                                         638
935
942
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                                                                                                                                                                                                                               ARM_REPEAT;
n transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., AND PHOSPHORYLATION SITE SER-942. PubMed=9478999;
                                                                               637
930
962
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942
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107906
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Primates;
  11.1%;
28.5%;
                                                                                      MW.
  Score
Pred.
                                                                                                                          GLOBULAR HEAD.
COILED COIL (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
PHOSPHORYLATION.
                                                                                                       S->A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                               Golgi stack;
                                                                                                                                                                                                                                                       UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takami N.,
                                                                                   A: LOSS OF PHOSPHORYLATION 2E748F2C1BC2B942 CRC64;
99;
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                                                                                                                                                                                                                                                                                                                                                                                                                There are no rest
  DB
1.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ikehara
                     1;
                                                                                                                                                                                                                                 Membrane; Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                              Usage
                   Length 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           а Y.;
р115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration
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RESULT 6
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                                                                                                                                                                                                                          Cell 33:575-563(1505).

-!- FUNCTION: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
-!- SUBBURIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILS.
-!- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
-!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE COITT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986
21-JUL-1986
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDILINE-83273600; PubMed-6576334;
MEDILINE-83273600; PubMed-6576334;
Karn J., Brenner S., Barnett L.;

"Protein structural domains in the Caenorhabditis elegans
myosin heavy chain gene are not separated by introns.";

Proc. Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).
                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell 33:575-583(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The genes sup-7 X and sup-5 III of C. \varepsilon nonsense mutations via altered transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McLachlan A.D., Karn J.;
"Periodic charge distributions
"periodic spacings in
match cross-bridge spacings in
Nature 299:226-231(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 850-1966 FROM MEDLINE=82272395; PubMed=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myosin heavy chi
UNC-54 OR MYO-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wills N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1876-1966 FROM MEDLINE=83232892; PubMed=65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYSB_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                853 LLQ 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 739
                                                                                               SIMILARITY: CONTAINS
                                                                                                                        MISCELLANEOUS: MHC A AND MHC B ARE WALL MUSCLE. THEY CO-ASSEMBLE INTO
                                                                                                                                                                            MISCELLANEOUS:
C.ELEGANS.
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELATLKSQLNSQSVEITKLQTEKQELLQKTEAFAKSVEVQGETETIIATKTTDVEGRLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VMECRNVTHLLQQELTEAQKGFQDVE-AQAATCNHTVMALMASLDAEKAQGQKKVEELEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EITTLNHKLQDASAEVERLRRENQ-VLSVRIADKKYYPSSQDSSSAAAPQLLIVLLGLSA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEELKRNQELLQSQLTEKDSMIENMKSSQTSGTNEQSSAIVSARDSE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gesteland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 01, Created)
(Rel. 01, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chain B (MHC B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1966 FROM N.A.
PubMed=6571695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           966 FROM N.A.
PubMed=7202124;
                                                                                                                                                                                                      THERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.F., Karn J.,
                                                                                                 1 MYOSIN-LIKE
                                                                                                                                                                                                   ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in the muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . elegans
er RNA.";
                                                                                                                        BODY WALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update
                                                                                                 GLOBULAR HEAD DOMAIN.
                                                                                                                           EXCLUSIVELY IN THE WALL THICK FILAMENT.
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Best Local S
Matches 36
                                                                                                                    NYH4_RABIT STANDARD; PRT; 1938 AA.

Q28641;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, skeletal muscle, juvenile.
                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
NP_BIND
                                                                                                                                                                                                                        1928
                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
 "Isolation, sequencing of myosin heavy chain cDNA from rabbit skeletal muscle and a novel cosynthesis of S-1 fragment with the essential and regulatory light chains.";
                               SQUENCE FROM N.A.
STRAIN-NEW ZEALAND WHITE; TISSUE-Skeletal mus
                                                                                                 Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; C
                                                                                                                                                                                                                                                               1871 KNFERLQDLIDKLQQKLKTQKKQVEEAE-ELANLNLQKYKQLTHQLEDAEERAD--QAEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding; Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00242; MYSC; 1.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J01050; AAA
EMBL; V01494; CAA
PIR; A02992; MWKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                              Maeda K., Hostin
Wittinghofer A.;
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004009; myosin_N.
InterPro; IPR002928; myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                               NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                       1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISSP; P08799;
                                                                                                                                                                                                                                           142 QVLSVRI---ADKKYYPSSQDSSSAA
                                                                                                                                                                                                                                                                                    107
                                                                                                                                                                                                                                                                                                                         47 KANSEACRDGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEK 106
                                                                                                                                                                                                                        SLSKMRSKSRASASVAPGLQSSASAA 1953
                                                                                                                                                                                                                                                                                                       EAEAAALKGGKKVIAKLEQRVRELESELDGEQRRFQDANKNLGRADRRVRELQFQVDEDK
                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                851
1165
1165
177
665
769
128
705
1337
11880
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA28124.1; -. CAA24738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                        1880
                                                                                                                                                                                                                                                                                                                                                                                                                   850
1966
1164
1176
1966
1968
184
687
783
128
705
715
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                                                                                                                                                                                                                                                                                                                                                       11.18;
24.78;
                                                                                                                                                                                                                                                                                                                                                                                              28 METHYLATION (TRI-) (POTENTIAL).

55 ALKYLATION (SH-1).

15 ALKYLATION (SH-2).

37 E -> R (IN REF. 2).

80 I -> L (IN REF. 2).

225125 MW; B66F0BB2FE27B67F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alkylation;
                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYOSIN HEAD-LIKE.
COILED COIL (POTENTIAL).
ALPHA-HELICAL TAILPIECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIGHT MEROMYOSIN (LM ATP (BY SIMILARITY).
                                                                                                   Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                           164
                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                       98.5;
No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROMYOSIN (LMM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multigene family.
                                                                                                                                                                                                                                                                                                                                                        .
2:
                                      muscle;
A., Schuster H.,
                                                                                                                                                                                                                                                                                                                                                                DΒ
                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                  -HKLQDASAEVERLRREN 141
                                                                                                                                                                                                                                                                                                                                                               Length 1966;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (S2).
                                       Gasperik
                                                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                       1870
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Best Local
                                                                                                                               Matches
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MOD_RES
MOD_RES
MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                          DOMAIN
MOD_RES
           1475
                                                                                         1366
                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U32574; AAA74199.1; -. HSSP; P08799; 1MMD.
                                                                                                                                                                                                                                                                                                               Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01576;
                                                                                                                                                                                                                                                                                                                                                                                                        Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                           Calmodul
                                                                                                                                                                                                                                                                                                                                   Myosin; Muscle protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                              139
                                                                     100
                                                                                                           47
                                                                                                           KANSEACR -----
                              RENOVLSVRIAD-KKYYPSSQD
           KESRSLSTEVFKVKNAYEESLD
                                                                     ASLDAEKAQGQKKVEELEGEITTLN----
                                                                                                                                                                                                                                                                                                                                                                                                                 PF00612; IQ; PF00063; myo:
                                                                                                                                                                                                                                                                                                                                                                                            PF02736; Myosin_N; 1. PF01576; Myosin_tail; 1.
                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                        in-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR004009; Myosin_N.
IPR002928; Myosin_tail.
IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000048;
                                                                                                                                                                                                   760
760
35
130
552
756
698
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 myosin_head; 1.
                                                                                                                                                                                 AA;
                                                                                                                                                                                                  783
1938
1938
186
680
774
35
130
552
756
                                                                                                                                                                                                                                                                                                                         ATP-binding;
                                                                                                                                         11.0%;
26.1%;
                                                                                                                                                                                 223064
                                                                                                                                                                                                                                                                                                                                   Coiled
                                                                                                                               20;
                                                                                                                                                                                 ₩.
                                                                                                                                       Score 98;
Pred. No.
                                                                                                                               Mismatches
                                                                                                                                                   DB
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-!- FUNCTION: MUSCLE CONTRACTION.
-!- SUBUNIT: MUSCLE CONTRACTION.
-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
--- AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
--- AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
--- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
--- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
--- CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
--- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN DE CAN BE SPLIT INTO 1 LIGHT MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN DE CAN BE SPLIT INTO 1 LIGHT MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN DE CAN BE SPLIT INTO 1 LIGHT MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN DE CAN BE SPLIT INTO 1 LIGHT MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN DE CAN BE SPLIT INTO 1 LIGHT MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN DE CAN BE SPLIT INTO 1 LIGHT MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN DECLARED BE CAN BE SPLIT INTO 1 LIGHT MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN DECLARED BE CAN BE SPLIT INTO 1 LIGHT MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN DECLARED BE CAN BE SPLIT INTO 1 LIGHT MYOSIN HEAVY CHAIN CHAIN CAN DECLARED BE CAN BE SPLIT INTO 1 LIGHT MYOSIN HEAVY CHAIN 
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-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1995)
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                                                                                                                                                                                                                      KANSEVAQWRTKYETDAIQRTEELEEAKKKLAQRLQDAE---EHVEAVNAKC-
/EDLMIDVERTNAACAALDKKQRNFDKILAEWKHKYEETHAELEASQ
                                                                                                                                                                                                                                                                                                                                       -DGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALM
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ATP (POTENTIAL).

ACTIN BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

METHYLATION (TRI-) (BY SIMILARITY).

METHYLATION (TRI-) (BY SIMILARITY).

METHYLATION (TRI-) (BY SIMILARITY).

ALKYLATION (SH-1) (BY SIMILARITY).

ALKYLATION (SH-2) (BY SIMILARITY).

ALKYLATION (SH-2) (BY SIMILARITY).

ALKYLATION (SH-2) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYOSIN HEAD-LIKE IQ.
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g; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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ROD-SHAPED
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RA Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

C -!- FUNCTION: MUSCLE CONTRACTION.

-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

ERAVY CHAIN SUBUNITS (MIC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

C AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

C -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

C -!- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE PHARXNGEAL MUSCLE.

C -!- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE PHARXNGEAL MUSCLE.

C -!- DOMAIN: THE ROLLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

C -- COMPANI: THE ROLLIKE TOR ALPHA-HELICAL COILED COILS.

C -- PARK: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

-- PARK: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

-- PARK: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

-- PARK: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE ACCOUNTY.

-- PARK: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND AND AND A HEAVY MEROMYOSIN (HMM), IT CAN LATER BE CONTROLLED TO THE COUNTY.

-- PARK: TWO CYSTEINE RESIDUES AND AND AND A HEAVY MEROMYOSIN (HMM), IT CAN LATER BE COUNTY.

-- PARK: TWO CYSTEINE RESIDUES AND AND AND A HEAVY MEROMYOSIN (HMM), IT CAN LATER BE COUNTY BEAVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83273600; PubMed-65/0334, MEDLINE-83273600; PubMed-65/0334, Karn J., Barener S., Barnett L.; Rarn J. Brenner S., Barnett L.; "Protein structural domains in the Caenorhabditis elegans unc-54 myosin heavy chain gene are not separated by introns."; myosin heavy chain gene are not separated by introns."; "> Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).
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21-JUL-1986 (Rel
01-OCT-1989 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
STRAIN-BRISTOL N2;
MEDLINE-89178677; PubMed-2926820;
MEDLINE-89178677; PubMed-2926820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYSD_CAEEL
P02567; Q1
                                           EMBL;
                                                            EMBL;
                                                                                                        EMBL;
                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed; entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                    the
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                                                                                EMBL;
                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                         C.ELEGANS.
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Karn J., Dibb N.J., Miller D.M.;
"Cloning nematode myosin genes.";
Cell Muscle Motil. 6:185-237(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin heavy chain D (MHC MYO-1 OR R06C7.10. Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                           -!- MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 34-1795 FROM N.A. MEDLINE-83273600; PubMed-6576334;
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01-OCT-1989 (Rel. 12, Last sequence upon 16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                 ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                               SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).
                                         X08065;
M37232;
M37234;
Z71266;
CAA95848.1;
CAA95848.1;
CAA95806.1;
                                                            CAA30854.1;
AAA28119.1;
AAA28120.1;
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Best Local
                              Eukaryota;
Pterygota;
Sciaridae;
                                                                                 01-AUG-1991
01-AUG-1991
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PUFF II/9-2
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SEQUENCE
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SEQUENCE FROM N.A
                   NCBI_TaxID=38358,
                                                             Sciara coprophila (Fungus
                                                                         11/9-2.
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SMART; SM00242; MYSC; 1.

Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Myosin; Multigene family.

ATP-binding; Methylation; Alfylation; Myosin HEAD-LIKE.

MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WormPep; R06C7.10; CE06253.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
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Pfam; PF00063; myosin_head;
                                                                                                                                                                                                              164 AAPQLLIV
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                                                                                                                                                                                                                                                       AEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSA 163
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                                                                                                                                                                                                                                   GEGLVGSEELEELKRKQMNRVMDLQEALSAA-----QNKVISLEKAKGKLLAETEDARSD 1438
                                                                                                                                                                                                                                                                                            EACRDGLRAVME----CRNVTHLLQQ--ELTEAQ-KGFQDVEAQAATCNHTVMALMASLD 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF01576; MyOSIN_N; 1.
PF01576; MyOSIN_tail; 1.
S; PR00193; MYOSINHEAVY.
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                                                                                                                                                                                                                                                                                                                               Similarity
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                               Bradysia.
                                                   ophila (Fungus gnat).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                        Neoptera;
                                                                                  protein precursor
                                                                                           (Rel. 19, Created)
(Rel. 19, Last sequence up
(Rel. 40, Last annotation
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                                        Endopterygota; Diptera;
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26.6%;
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DV -> GD (IN REF. 2).
V -> D (IN REF. 4).
W -> N (IN REF. 2).
C -> G (IN REF. 2).
L -> F (IN REF. 4).
I -> N (IN REF. 4).
S -> D (IN REF. 2).
C -> C (IN REF. 3).
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Pred. No. 4
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D ≈ E
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ALKYLATION (SH-1).
ALKYLATION (SH-2).
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ATP (BY SIMILARITY).
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ALPHA-HELICAL TAILPIECE (SHORT S2)
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                                         Nematocera; Sciaroidea;
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P41542;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
CARBOHYD
                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
General vesicular transport factor pl15 (Transcytosis associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                protein) (TAP) (Vesicle docking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities re
or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coprophila.
         SEQUENCE FROM N.A.,
                                            endoplasmic
                                                       Waters M.G.;
"p115 is a general vesicular transport factor related
                                                                              Sapperstein S.K.,
                                                                                         MEDLINE-95132632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dibartolomeis S.M.,
                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                         Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90133907; PubMed=2614832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dibartolomeis S.M., Gerbi S.A.; Molecular characterization of DNA
                                                                                                                                                                                                                                                                                                                                198
                                                                                                                                                                                                                                                                                                                                                       147
                                                                                                                                                                                                                                                                                                                                                                              143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AOI. Biol. 210:531-540(1989).

MISCELLANEOUS: THE DNA PUFF II/9 PROTEINS HAVE A PROPOSED INTERMOLECULAR COILED COIL STRUCTURE WITH POSSIBLY INTERMOLECULAR DISULFIDE BRIDGES FORMED BY NUMEROUS CYSTEINE RESIDUES IN POSITION DOF THE HEPTAD REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     x51679;
s07533; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                       ×
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                                                                                                                                                                                                                                                                                                                                                                            ----KENAKLINKIEELNCTITQLQEKLERCRGRERDLQCQLDECKKKLNICNNELIAC
                                                                                                                                                                                                                                                                                                                                                                                                                                           IKANSEACRDGLRAVMEC-RNVTHL-----LQQELTEAQKGFQDVEAQAATCNHTVMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                           LKREKEARQKAEKALKECQKNTENLKETIEQLKKELAEAQKALEKCKKELADCK-----
                                                                                                                                                                                                                                                                                                                                                                                                     MASLDAEKAQGQKKVEELEGEITTLNHKLQ------DASAEVERLRRE-----NQVLSV 146
                                 Natl.
                                                                                                                                                                                                                                                                                                                                198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                   Eutheria;
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20
61
156
286 AA;
                               reticulum
Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAA35982.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coil; Glycoprotein.

1 19 OR 21 (POTENTIAL).

0 286 PUFF II/9-2 PROTEIN.

1 235 HELICAL (POTENTIAL).

6 156 N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76% IDENTICAL TO THE PUFF II/9-1 PROTEIN.
                                                                            PubMed=7831323;
Walter D.M., Grosvenor A.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286
235
156
156
32621 MW;
                                                                                                                                                  Rodentia;
         AND PARTIAL
                                                                                                                                                               Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.9%;
                               to Golgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                               i transport factor 92:522-526(1995).
                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                  Sciurognathi;
                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                720AC8CCC22A869C CRC64;
           SEQUENCE
                                                                                                                                                                                                protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   puff II/9A genes
                                                                                                                                                                                                                                                                       959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
0.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are
                                                                                                                                                                                                                                                                      A
                                          factor Usolp.";
                                                                                                                                                  Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 286
                                                                              Heuser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                  Murinae; Rattus
                                                       ç
                                                                              J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sciara
                                                     the yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                            197
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RESULT 11
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                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
YM92_CAEEL . STANDARD;
P34531; P34532; P34533;
01-FEB-1994 (Rel. 28, Cres
01-FEB-1996 (Rel. 33, Las
01-MAR-2002 (Rel. 41, Las
                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPKUUU222, ...
PROSITE; PS50176; ARM_REPEAT;
Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor required for binding of vesicles to acceptor membranes.";
Proc. Natl. Acad. Sci. U.S.A. 92:527-531(1995).
-!- FUNCTION: GENERAL VESICULAR TRANSPORT FACTOR REQUIRED FOR
-!- INTERCISTENAL TRANSPORT IN THE GOLGI STACK; IT IS REQUIRED FOR
TRANSCYTOTIC FUSION AND/OR SUBSEQUENT BINDING OF THE VESICLES THE TARGET MEMBRANE. MAY WELL ACT AS A VESICULAR ANCHOR BY
INTERACTING WITH THE TARGET MEMBRANE AND HOLDING THE VESICULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U14192; AAA62632.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Transcytosis-associated protein (TAP)/pll5 is a general fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barroso M., Nelson D.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95132633; PubMed=7831324;
                                                                                                                                  853
                                                                                                                                                              178
                                                                                                                                                                                            793
                                                                                                                                                                                                                           119
                                                                                                                                                                                                                                                       739
                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN WHICH RECYCI BETWEEN THE CYTOSOL AND THE GOLGI APPARATUS DURLING INTERPHASE DOMAIN: COMPOSED OF A GLOBULAR HEAD, AN ELONGATED TAIL (COILEI COIL) AND A HIGHLY ACIDIC C-TERWINAL DOMAIN.

PTM: PHOSPHORYLATED IN A CELL CYCLE-SPECIFIC MANNER;
PHOSPHORYLATED IN INTERPHASE BUT NOT IN MITOTIC CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE, PHOSPHORYLATION PROMOSTES DISSOCIATION (BY SIMILARITY). SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND TARGET MEMBRANES IN PROXIMITY.
SUBUNIT: HOMODIMER WITH TWO N-TERMINAL HEADS AND A C-TERMINAL
COILED-COIL TAIL. DIMER FORMED BY PARALLEL ASSOCIATION OF THE
                                                                                                                                 DIT
                                                                                                                                                              LLQ 180
                                                                                                                                                                                                                        EITTLNHKLQDASAEVERLRRENQVLSVRIAD-KKYYPSSQDSSSAAAPQLLIVLLGLSA 177
                                                                                                                                                                                                                                                    IEELRSHQVLLQSQLAEKDTVIENLRSSQVSGMSEQALATCSPRDAE-----QVAELKQ
                                                                                                                                                                                                                                                                                 VMECRNVTHLLQQELTEAQKGFQDV-EAQAATCNHTVMALMASLDAEKAQGQKKVEELEG
                                                                                                                                                                                            ELSALKSQLCSQSLEITRLQTENSELQQRAETLAKSVPVEGESELVTAAKTTDVEGRLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U15589;
                                                                                                                                                                                                                                                                                                                37;
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                  855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000225; Armadillo.
(Rel. 28, Created)
(Rel. 33, Last sequence up)
(Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                      638
935
940
591
658
816
873
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC52151.1;
                                                                                                                                                                                                                                                                                                                                                                                                       637
930
959
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816
                                                                                                                                                                                                                                                                                                                             10.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                   GLOBULAR HEAD.
COILED COIL (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
PHOSPHORYLATION (BY SIMILARITY).
S -> P (IN REF. 2).
M -> V (IN REF. 2).
S -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                             Score 97; DB
Pred. No. 2.6;
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNKNOWN_1.
Golgi stack;
                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                         356394B48C7E003B
                                                         893
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2.6;
                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Membrane;
                                                                                                                                                                                                                                                                                                                58;
                                                                                                                                                                                                                                                                                                                                           Length 959
                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions
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Best Local
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PU91_SCICO STANDARE
P23311;
01-AUG-1991 (Rel. 19, C
01-AUG-1991 (Rel. 19, I
16-OCT-2001 (Rel. 40, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                               SCICO
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S40998; S40998
PIR; S40999; S40999
WormPep; M01A8.2; CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000938; CAP-Gly. Pfam; PF01302; CAP_GLY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical 100.0 kDa M01A8.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "2.2 Mb of contiguous nucleotide sequence from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans
                                                                                                                                         685
                                                                                                                                                                     140
                                                                                                                                                                                                   625
                                                                                                                                                                                                                               102
                                                                                                                                                                                                                                                             566
                                                                                                                                                                                                                                                                                          48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                             SNQQVIRNHANAV-ESLQKTHETQIAEKNKEFERNFEEERARREAEVCAMNNRHQKVVAC
                                                                                                                                         KNQNLSLQV
                                                                                                                                                                   ENQVLSVRI
                                                                                                                                                                                                                               LDAEKAQGQKKVEELE--
                                                                                                                                                                                                                                                                                       ANSEACRDGLRAVMECRNVTHLLQ--QELTEAQKGFQDV----EAQAATCNHTVMALMAS
                                                                                                                                                                                                 LDEKISEAEKQCEQLNVDKKVLQAALANDCDHRNQMLTKEISSLQTALEMKSAEMKELRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z27081; CAA81607.1;
                                                                                                                                                                                                                                                                                                                        32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                           PS00845; CAP_GLY_1; 1.
PS50245; CAP_GLY_2; 1.
:1cal protein; Coiled coil.
39 81 CAP-GLY.
522 696 COILED COIL (POTENTIAL).
729 756 COILED COIL (POTENTIAL).
893 AA; 99997 MW; 464F2962B36C28B1 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requires
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                         693
                                                                                                                                                                   148
                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONTAINS 1 CAP-GLY DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CE03491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                   10.9%;
 Created)
Last sequence
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein M01A8.2
   sequence up
annotation
                                                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                     Score 96.5; D
Pred. No. 2.6;
29; Mismatches
                 update)
                                                                286
                                                                                                                                                                                                                                                                                                                                      .
6.
                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                               -GEITTLNHKLQDASAEVERLRR
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                                                                                                                                                                                                                                                                                                                      39;
                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            III of
                                                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                     Gaps
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20
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular characterization coprophila.";
J Mol nici
                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. MOI.
         TISSUE=Skeletal muscle;
MEDLINE=90323631; PubMed=2373371;
Karsch-Mizrachi I., Feghali R., Shows T.B. Ji
"Generation of a full-length human perinatal
encoding cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                          P13535, Q14910;
01-JAN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sciaridae; Bradysia.
NCBI_TaxID=38358;
                                                                  SEQUENCE FROM N.A.
                                                                                                                                                Myosin
                                                                                                                                                                                                        MYH8_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90133907; PubMed=2614832; Dibartolomeis S.M., Gerbi S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-6980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUFF II/9-1 protein precursor.
                                                                                                                                                                                                                                                                158
                                                                                                                                                                                                                                                                                                           102
                                                                                                                                                                                                                                                                                    119 EITTLNHKLQDASAEVERLR
                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D OF THE HEPTAD REPEAT. SIMILARITY: 76% IDENTICAL TO THE PUFF II/9-2 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISCELLANDOUS: THE DNA POFF II/9 PROTEINS HAVE A PROPOSINTERMOLECULAR COILED COIL STRUCTURE WITH POSSIBLY INTE DISULFIDE BRIDGES FORMED BY NUMEROUS CYSTEINE RESIDUES D OF THE HEPTAD REPEAT.
                                                                                                                                                                                                                                                                                                                                 AVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEG
                                                                                                                                                                                                                                                              TITQLQEELEQCRARERDLQ
                                                                                                                                                                                                                                                                                                           ALCECQKNSELLKQTIEQLKKELAQTKQELANCKEA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X51680; CAA35983.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
289-294(1990)
                                                                                                                                                                                                                                                                                                                                                                                                            20
61
156
286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ophila (Fungus gnat).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Trachera; Rematocera; Scia
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                           (Human)
                                                                                                                                                chain,
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                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             1; Glycoprotein.
19 OR 21 (POTENTIAL).
286 PUFF II/9-1 PROTEIN.
235 HELICAL (POTENTIAL).
156 N-LINKED (GLCNAC. . .) (F
32034 MW; AA6A7B55F191BB1D CRC64;
                                                                                                    Chordata;
Primates;
                                                                                                                                                skeletal muscle,
                                                                                                                                                                                                                                                                                                                                                                 10.8%;
                                                                                                                                                          sequence up
                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of DNA
                                                                                                                                                                                                                                                                                                                                                                 Score 96; I
                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      puff II/9A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    It is produced
                                                                                                                                                                       update)
                                                                                                                                                                                                         1937
                                                                                                                                                perinatal
                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                   DB 1;
0.84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no
                                Jr.,
                                                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as its content
                      myosin heavy-chain-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                           LANCKAENAKLLKKIEELNC 157
                                                                                                                                                                                                                                                                                                                                                         36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes
                                                                                                                                                (MyHC-perinatal).
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                                  Leinwand
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                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
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                                L.A.
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L outstation -
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EMBL; M36769; AAC17185.1; -. EMBL; Z38133; CAA86293.1; -. EMBL; X51592; CAA35941.1; -. EMBL; M35250; AAA36346.1; -. EMBL; AF067143; AAC21557.1; -. PIR; A30220; A30220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE T
                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bober E.,
Arnold H.
                         Pfam; PF00063; myosin_head; 1. Pfam; PF02736; Myosin_k; 1. Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

TISSUB--Skeletal muscle;

MEDLINE-95324556; pubMed-7601129;

Jullian E.H., Kelly A.M., Pompidou A.J., Hoffman R.,

Stedman H.H., Rubinstein N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESSET K., Tidhar A., Myszkowski M.; "Isolation and characterization of the human p Submitted (MAY-1998) to the EMBL/GenBank/DDBJ-I- FUNCTION: MUSCLE CONTRACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of three developmentally controlled isoforms of myosin heavy chains.";
                                                                                       InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; Myosin_head.
                                                                                                                                                           HSSP; P08799; 1LVK...
MIM; 160741; -.
                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                        This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human perinatal myosin heavy chain.";
J. Cell Biol. 108:1791-1797(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feghali R., Leinwand L.A.;
Molecular genetic characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 860-1937 FROM N.A. MEDLINE=89234168; PubMed=2715179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90235862; PubMed=1691980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 502-1937 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of a human perinatal myosin heavy-chain transcript.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA HELICAL COILED COILS.
CHARACTERISTIC FOR ALPHA HELICAL COILED COILS.
PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASES ACTIVITY
MISCELLANBOUS: BACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBERRAGMENTS (S1) AND 1 ROD-SHAPED
STRUEDRAMMENT (S2).
                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBI European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBFRAGMENT (S2)
                                                                           PF00612; IQ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. 189:55-65(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. 230:1001-1006(1995).
PD000355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchberger-Seidl A., Braun T., Singh S., Goedde
               MYOSINHEAVY
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                                                                                                                                                                                                                                                                                                                       http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                      EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                   collaboration
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Best Local S
Matches 33
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CONFLICT
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                                                                                                                                                                                              MYHB.HUMAN STANDARD; PRT; 1972 AA P35749; 000396; P78422; 094944; 01-JUN-1994 (Rel. 29, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, East annotation update) MyOsin heavy Chain, smooth muscle isoform (MYH11 OR KIAA0866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
          SEQUENCE OF 1-1266 FROM TISSUE=Brain;
                                        Loftus B.J., Kim U.-J., Sneddon V.P., Kalush R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., M. Eichler E.E., Harris P.C., Venter J.C., Adams M.D. "Genome duplications and other features in 12 Mb. human chromosome 15p and 16q."; Genomics 60:295-308(1999).
                                                                                                   SEQUENCE FROM N.A.
MEDLINE=99425270; PubMed=10493829;
MEDLINE=99425270; Sneddon V.P.,
                                                                                                                                                                                                                                                                                                                                                                                                             1366
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ATP-binding; Me
MEDLINE=99156230; PubMed=10048485;
                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                           150
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                                                                                                                                                                                                                                                                                                                                                                                                                                KANSEACR------DGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALM
                                                                                                                                                                                                                                                                                                                                                                 NEVEDLMLDVERSNAACAALDKKQRNFDKVLSEWKQKYEETQAELEASQKESRSLSTELF
                                                                                                                                                                                                                                                                                                                                                                                    ----ASLDAEKAQG-----QKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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1072
1247
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1847
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Methylation; Alkyl
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1847
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1937
188
680
774
132
698
708
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Primates;
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                     N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
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ALKYLATION (SH-1) (I
ALKYLATION (SH-2) (I
A-> R (IN REF. 2).
E-> Q (IN REF. 1 AN
M-> N (IN REF. 3).
N-> H (IN REF. 3).
N-> H (IN REF. 1 AN
MC-> DGG (IN REF. 1 AN
E-> G (IN REF. 1 AN
K -> Q (IN REF. 1 AN
K -> Q (IN REF. 1 AN
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Pred. No.
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ATP.
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                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coil; Thick filament; Ac
lation; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A3EE2D151792E9E8 CRC64;
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H (IN REF. 2)
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AND 4).
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M., Cronin
, Mitchell
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-i- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
-i- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-i- TISSUE SPECIFICITY: SMOOTH MUSCLE; EXPRESSED IN THE UMBILICAL ARTERY, BLADDER, ESOPHAGUS AND TRACHEA.
-i- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CYCLES OF A 28-RESIDUES IN THE SID DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
-i- PYM: TMO CYSTERINE RESIDUES IN THE SID DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
-I- DISSASE: A CHROMOSOMAL REARRANGEMENT, KNOWN AS PERICENTRIC INVERSION INV(16) (P13022), PRODUCES A FUSION PROTEIN THAT CONSISTS OF THE 165 N-TERMINAL RESIDUES OF CBF-BETA (PEPB2) WITH THE TAIL RESIDUE DIEUKEMIA OF M4EO SUBTYPE.
-I- MISCELLAMEDUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN CAN BE SPLIT IN
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Alkylation; Multigene family; Proto-oncogene; Chromosomal translocation.
                                                                                                                                                       SMART; SM00015; IQ; 2.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                           Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics
the European Bioinformatics Institute. There a
use by non-profit institutions as long as i
modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF001548; AAC31665.1; -. EMBL; U91323; AAC35212.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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Yanagisawa M., Masaki T., Takao A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF
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Miyajima N.,
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SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nitted (NOV-1992) to the EMBL/GenBank/DDBJ databases FUNCTION: MUSCLE CONTRACTION.
SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00612;
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                                                                                                                       PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000048; IQ.
IPR002928; Myosin_tail.
IPR002017; Spectrin.
IPR001609; myosin_head.
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RESULT 15
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Best Local S
Matches 27
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                                                                                          Proc. Natl. Acad. SCI. CONTRACTION.

-!- FUNCTION: MUSCLE CONTRACTION.

-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC-2).

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILS.

-!- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

-!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT TOWN AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                       gene: complete nucleotide and protein coding sequence the 5' end of the gene.";
Proc. Natl. Acad. Sci. U.S.A. 88:10676-10680(1991).
                                                                                                                                                                                                                                                                                            MEDLINE=92073350; PubMed=1961735;
Babij P., Kelly C., Periasamy M.;
"Characterization of a mammalian smooth muscle myosin
                                                                                                                                                                                                                                                                                                                                                                                MYH11.
Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Capbit).
Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1268
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                               Myosin heavy MYH11.
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 CRDGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLD-----
                                                 SIMILARITY: CONTAINS SIMILARITY: CONTAINS
                                                                            SUBFRAGMENT (S2)
                                                                                     MEROMYOSIN (LMM) AND
SPLIT FURTHER INTO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSDGERARAELNDKVHKLQNEVESVTGMLNEAEGKAIKLAKDVASLSSQLQDTQELLQEE 1327
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27; Conserv
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(Rel. 33, Last sequence update)
(Rel. 40, Last annotation updat
(Rel. 40, mooth muscle isoform (
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                                                                                      GLOBULAR
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                                                MYOSIN-LIKE IQ DOMAIN.
                                                                                     HEAVY MEROMYOSIN (HMM). I
LOBULAR SUBFRAGMENTS (S1)
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ALKYLATION (SH-2) (POTENTIAL).
EEK -> NSE (IN REF. 3).
ELOS -> TLSF (IN REF. 2).
T -> S (IN REF. 3).
KQ -> NE (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A -> S (IN REF. 4).
T -> L (IN REF. 3).
MW; 67665BB2AECE1277
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IQ.
COILED
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ACTIN-BINDING (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          isoform (SMMHC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1972 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                              GLOBULAR HEAD DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                        AND
                                                                                                                                                                                                                                                                                 and analysis
                                                                                                                                                                                                                                                                                               heavy-chain
                                                                                        ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103
                                                                                                                                                                                                                                                                                    of.
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SOUTH THE TENT OF 
                                                                                                                                                                                                                                                   Query Match 10.7%; Score 95; DB Best Local Similarity 24.5%; Pred. No. 8; Matches 27; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPRO00048; IQ.
InterPro; IPRO00048; IQ.
InterPro; IPRO02928; Myosin_tail.
InterPro; IPRO02017; Spectrin.
InterPro; IPRO02017; Spectrin.
InterPro; IPRO0169; myosin_head.
Pfam; PF00612; IQ; 1.
Pfam; PF00073; myosin_head; 1.
Pfam; PF002736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PF000355; myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
DOMAIN
DOMAIN
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
1328 TROKLNVSTKLROLEDERNSLQEQLDEEMEAKQNLERHISTLNIQLSDSK 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                            1268 CSDGERARAELNDKVHKLQNEVESVTGMLSEAEGKAIKLAKEVASLGSQLQDTQELLQEE 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A41604; A41604.
HSSP; P08799; 1MMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M77812; AAA31395.1; -.
                                          104 -AEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKK 152
                                                                                                                                                                                 53 CRDGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLD------ 103
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844
1935
178
661
763
129
701
711
1972
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807
1934
1972
185
683
777
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701
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

METHYLATION (TRI-) (POTENTIAL).

ALKYLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                          ALKYLATION (SH-2) (POTENTIAL).
MW; 2061A224288D6A4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYOSIN HEAD-LIKE.
IQ.
COILED COIL (POTENTIAL).
CARBOXYL-TERMINAL.
                                                                                                                                                                                                                                                                                                                    DB 1; Length 1972;
                                                                                                                                                                                                                                                         55;
                                                                                                                                                                                                                                                         Indels
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δÃ В QΥ Search completed: June 4, 2002, 15:28:13 Job time: 126 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2002, 15:25:07; Search time 16.33 Seconds (without alignments) 1059.160 Million cell updates/sec

Title: Perfect score: US-09-828-217-1 889

Sequence:

Gapop 10.0 , Gapext 0.5

Scoring table: BLOSUM62

1 MASTSYDYCRVPMEDGDKRC.....SSAAAPQLLIVLLGLSALLQ 180

Searched:

283138 seqs,

96089334 residues

otal number of hits satisfying chosen parameters:

283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* pir1:\*
pir2:\*
pir3:\*
pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

29	20	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	U	4	w	2	1	Result
93	و د	0 5	93.5	93.5	93.5	94	94.5	95	95	95.5	96	96.5	96.5	97	86	98	98	98.5	99	99.5	102	102.5	107	107.5	108	111	889	Score
10.5	10.5	10.5	10.5	10.5	10.5	•	•	10.7	10.7	10.7	10.8	10.9	10.9	10.9	11.0	11.0	11.0	11.1	11.1	11.2	11.5	11.5	;-		12.1	12.5		% Query Match 1
1938	870	9 7 9	1939	1938	140	676	1388	1972	1937	173	286	893	597	286	1938	1938	959	1963	415	304	550	1534	143	461	423	778	180	Length D
		) N	2	_	N	N	N	1						2	N		2					2	2	2	N	N	1	DB
JC5421	A48575	150712	148175	S06005	н64629	S00084	S74245	A41604	I38055	S76705	S07532	G88551	S40998	S07533	A59293	MWKW1	A55913	MWKW	S35760	JX0209	A28166	A56734	G83955	Н84099	I59463	T30430	A56836	ID
smooth muscle myos	paramyosin - nemat	10	myosin heavy chain		tical	myosin heavy chain	/threon			thetical	puff II/9-1 protei		thetical	puff II/9A-2 prote	skeletal myosin he	myosin heavy chain			fcrA protein precu	a	Kupffer cell recep		flagellar protein	cell wall-binding	keratin, type I, c	hypothetical prote	bone marrow stroma	ā

centrosome associa	T08621	N	2442	10.3	91.5	5
myosin alpha heavy	A46762	<u>_</u>	1939	10.3	91.5	14
myosin beta heavy	S06006	Н	1935	10.3	91.5	3
myosin beta heavy	A37102	سا	1935	10.3	91.5	2
myosin heavy chain	148153	Ν	1934	10.3	91.5	Ë
myosin heavy chain	S18199	N	1039	10.3	91.5	ö
myosin heavy chain	151302	N	764	10.3	91.5	39
beta-myosin heavy	136913	N	244	10.3	91.5	8
hypothetical prote	T19296	2	872	10.3	92	37
paramyosin - Caeno	S04027	N	866	10.3	92	8
myosin II heavy ch	T47237	Ν	746	10.3	92	5
alpha cardiac myos	I49464	Ν	1938	10.4	92.5	34
myosin heavy chain	A27224	μ.	1509	10.4	92.5	ü
general stress pro	В98124	2	392	10.4	92.5	32
secreted 45 kd pro	G95258	N	392	10.4	92.5	3
smooth muscle myos	JC5420	N	1972	10.5	93	ö
	•					

## ALIGNMENTS

RESULT 2 130430 hypothetical protein ORF82 - Lymantria dispar nuclear polyhedrosis virus C.Species: Lymantria dispar nuclear polyhedrosis virus, LdNNPV C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C.Accession: T30430 R.KUZiO, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; R Virology 253, 17-34, 1999 A.;Attle: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantri A.;Accession: T30430 A.;Accession: T30430 A.;Status: preliminary; translated from GB/EMBL/DDBJ A.;Molecule type: DNA	Db 1 MASTSYDYCRVPMEDGDKRCKLLLGIGILVLLIVILGVPLIIFIIHHIHHIHHIHHIHHIHHIHHIHHIHHIHHIHHIHH	A;Gene: GDB:BST2 A;Cross-references: GDB:409946; OMIM:600534 A;Cross-references: GDB:409946; OMIM:600534 A;Map position: 19p13.2-19p13.2 C;Reywords: transmembrane protein C;Reywords: transmembrane protein Query Match Query Match Best Local Similarity 100.0%; Score 889; DB 2; Length 180; Best Local Similarity 100.0%; Pred. No. 2.6e-62; Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 1 A56336  bone marrow stromal cell surface protein BST-2 - human C*Species: Homo sapiens (man) C.Date: II-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 21-Jul-2000 C;Accession: A56836 C;Accession: A56836 R;Ishikawa, J.; Kaisho, T.; Tomizawa, H.; Lee, B.O.; Kobune, Y.; Inazawa, J.; Oritani Genomics 26, 527-534, 1995 A;Title: Molecular cloning and chromosomal mapping of a bone marrow stromal cell surf A;Reference number: A56836; MUID:95331788 A;Accession: A56836 A,Scatus: preliminary; not compared with conceptual translation A;Rolecule type: mRNA A;Rolec
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A;Introns: 132/3; 160/2; 212/3; 267/3; 309/3; 384/2 C;Superfamily: cytoskeletal keratin C;Keywords: coiled coil; intermediate filament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:Y00217; NID:g50842; PIDN:CAA68365.1; R;Ichinose, Y.; Morita, T.; Zhang, F.; Srimahasongcram, S.; Gene 70, 85-95, 1988
A;Title: Nucleotide sequence and structure of the mouse cytc A;Reference number: JT0406; MUID:89196920
A;Accession: JT0406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-243, 'D', 245-252, 'A', 254-423 <SIN>
A; Cross references: GB:M11686; NID:9198620; PIN:AAA39390.1; PID:9293685
R;Oshima, R.G.; Trevor, K.; Shevinsky, L.H.; Ryder, O.A.; Cecena, G.
Genes Dev. 2, 505-516, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M36376; NID:g198587; PIDN:AAA39373.1; PID:g293682 R;Singer, P.A.; Trevor, K.; Oshima, R.G.
J. Biol. Chem. 261, 538-547, 1986
A;Title: Molecular cloning and characterization of the endo B cytokeratine, Reference number: A25621; MUID:86085876
A;Accession: A25621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-423 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ratin, type I, cytoskeletal - mouse
Alternate names: endo B cytokeratin; keratin D
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 10-Dec-1999
C;Accession: I59463; A25621; A28428; JT0406
R;Alonso, A.; Weber, T.; Jorcano, J.L.
Roux's Arch. Dev. Biol. 196, 16-21, 1987
A;Title: Cloning and characterization of keratin D, a murine endodermal cytoskeletal A;Reference number: I59463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
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8
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                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                              A;MoLecule type: DNA A;MoLecule type: DNA A;Residues: 1-133,'f';135-243,'D',245-252,'A',254-423 <ICH>A;Cross-references: GB:M22832; NID:g340757; PIDN:AAA37552.1 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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A; Cross-references: EMBL: AF081810; PIDN: AAC70268.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Identification of the gene coding A; Reference number: A28428; MUID:88255838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: I59463
                                                                                                                                                                                                                                                                                                                                                           A; Gene: endoB; KERD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: DNA
Residues: 1-132 <OSH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: A28428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 EKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSS
                                                  157 FRVKYETELAMRQSVESDIHGLRKVVDDTNITRLQLETEIEALKEELLFMKKNHEEEVQG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 IKANSEACRDGLRAVMECR-NVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
84 VEAQAATCNHTV
                                                                                                 44 FTIKANSE-ACRD-----GLRAVMECRNVTHL------LQQELTEAQKG----FQD
                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKAQSELNRD-LQAKAEAQADANARLQAEIDSLKR----AESDAADLRNRVAQLEAEAES 574
                                                                                                                                                      52;
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                                                                                                                                                      Conservative
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                                                                                                                                                                        12.1%;
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MALMASLDAE - KAQGQKKVEELE
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                                                                                                                                                Score 108; DB Pred. No. 0.44; Nismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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                                                                                                                                                      56; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    murine cytokeratin and its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID:g50843
Tondella, M.L.C.;
                                                                                                                                                                                                                                                                                                                                                                                                           PID:g532610
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     -GEIT 121
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C:Species: Bacillus halodurans (Strain C-125) (C;Species: Bacillus halodurans (Strain C-125) (C;Species: Bacillus halodurans (C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 (C;Accession: H84099 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132 A;Accession: H84099
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                                                                                                                                                                                                                                                                              A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07319.1; GSPDB:GA;Experimental source: strain C-125
C;Genetics:
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                                   Ş
                                                                            В
                                                                                                                Q
                                                                                                                                                                                                                                                             A; Gene: BH3600
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A; Residues: 1-461 <STO>
                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
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                                                                                                                                                            Matches
                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217
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  60
                                      93 HTVMALMASLDAEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADK 151
                                                                                                                  33 IIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCN 92
                                                                              5 ISLVAAAGLLTFSILFSQSSIEDA-KANSSLQNQISDVQKERQEKQQEKQKTEAEL---- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSS
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                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        342
                                                                                                                                                                             12.1%; Score 107.5; D
26.1%; Pred. No. 0.52;
                                                                                                                                                              28; Mismatches
                                                                                                                                                                                                  DB 2;
                                                                                                                                                              55;
                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SAAAPQLLIVLL 173
                                                                                                                                                              5.
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336
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RESULT G83955 γ R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nuclelc Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132 flagellar protein required for flagellar formation fliL [imported] - Bacillus halodur
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001
C;Accession: G83955 A; Gene: fliL A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06166.1; A;Experimental source: strain C-125 A; Molecule type: DNA A; Residues: 1-143 <STO> A; Accession: G83955 A;Status: preliminary Local Similarity 22. 23 LLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMEC-----12.0%; Score 107; DB 22.1%; Pred. No. 0.17; ative 34; Mismatches DB 2; 49; Length 143 Indels -- RNVTHLLQQEL 74 26; Gaps 4; GSPDB:G

В

6

LVNIMLIILIVLTLVGVAVLIFVNYFNNEDEQDREPTIDEIIAQSYETEEITTNLLSNDF 65



	RESULT 7 A28166 Kupffer cell receptor - rat C:Species: Rattus norvegicus (Norway rat) C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 05-Nov-1999 C:Accession: A38674; A28166 R:Hoyle, G.W.; Hill, R.L. Biol. Cham. 266, 1857, 1991 Title: Structure of the gene for a carbohydrate-binding receptor unique to rat Kupffer R:Accession: A38674; MUID:91107689 A:Accession: A38674 A:Status: preliminary A:Molecule type: DNA A:Residues: 1-550 <ho2> A:Cross-references: GB:M55532; NID:g203362; PIDN:AAA40892.1; PID:g203363 R:Hoyle, C.W.; Hill, R.L.</ho2>	Oy 127 LODASABUVELREMOVLSV 146  Db 119 LODDINALMOEGSVVKI 135  RESULT 6 A56734 ribosome receptor, 180k - dog C:Beccies: Canis lupus familiaris (dog) C:Cancession: A56734 R:Manker, E.E.; Sun, Y.; Savitz, A.J.; Meyer, D.I. J. Cell Biol, 130, 29-39, 1995 A.Filte: Functional characterization of the 180-kD ribosome receptor in vivo. A:Reference number: A56734; MUID:95310363 A:Accession: A56734 <anna (n-q-g-k-k-a-e-g-a-p)="" 1-1534="" 10-residue="" 114="" 115="" 144="" 1;="" 22;="" 26;="" 28.6%;="" 4.4;="" 42;="" 55="" 847="" 906="" :::: ="" <anna="" a:coss-references:="" a:residues:="" best="" blosynthesis="" c:reywords:="" conservative="" daavaksklrevnkelaaekakaageakvkkqlvareqeitavqarieasyrehvkevo="" db="" dlrammernuthlloelteaokgfodvaaatcnhtwalmasldaekagogkve="" elegeittlnhklqda-saeverlarenqvl="" endoplasmic="" f:198-743="" gaps="" gb:x87224;="" hasthess="" indels="" local="" match="" membrane="" mismatches="" nid:9984113;="" no.="" ouery="" oy="" pid:9984114="" pidn:caa66676.1;="" pred.="" protein="" protein;="" region:="" repeats="" reticulum;="" similarity="" th=""  =""  <=""><th>Qy 75 TEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEITTLNHK 126  </th></anna>	Qy 75 TEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEITTLNHK 126
RESULT 9 \$35760  forA protein precursor - Streptococcus pyogenes C;Species: Streptococcus pyogenes C;Species: Streptococcus pyogenes C;Date: 13-Jan-1995 **sequence_revision 13-Jan-1995 **text_change 26-Aug-1999 C;Accession: \$35760; A42711 R;Podbielski, A. submitted to the EMBL Data Library, November 1992 A;Reference number: \$35760 A;Accession: \$35760 A;Accession: \$35760 A;Accession: \$35760 A;Accession: \$35760 A;Accession: \$1415 <pod> A;Cross-references: EMBL:X69324; NID:9311759; PIDN:CAA49165.1; PID:9311760 A;Cross-references: EMBL:X69324; NID:9311759; PIDN:CAA49165.1; PID:9311760 R;Haanes, E.J.; Heath, D.G.; Cleary, P.P.</pod>	Query Match  Best Local Similarity 23.2%; pred. No. 1.4;  Best Local Similarity 23.2%; pred. No. 1.4;  Matches 36; Conservative 37; Mismatches 49; Indels 33; Gaps  Qy 24 LGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQELTEAQKGF 81    :: ::::	Qy 106 KAQGOKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSAAA 165	Qy 46 IKANSBACRDGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAE 105

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references: GB:S36676; NID:g249360; PIDN:AAB22171.1; PID:g249361
3.; Sato, M.; Toyoshima, S.; Osawa, T.
nem. 104, 600-605, 1988

Purification and characterization of a lectin-like molecule specific for since number: PX0009; MUID:89197865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           galactose/N-acetylgalactosamine-specific - mouse
ss: Mus musculus (house mouse)
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
ion: JX0209; PX0009
M.; Kawakami, K.; Osawa, T.; Toyoshima, S.
hem. 111, 331-336, 1992
: Molecular cloning and expression of cDNA encoding a galactose/N-acetylgalact
ence number: JX0209; MUID:92268032
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                                                                                                                                                                                                                                                                                                                                                                          match 11.2%; Score 99.5; DB 2; Length 304;
.ocal Similarity 23.2%; Pred. No. 1.4;
.s 36; Conservative 37; Mismatches 49; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ile type: protein
les: 102-120;137,'X',139-151 <ODA>
les: 102-120;137,'X',139-151 <ODA>
lamily: hepatic lectin; C-type lectin homology
ds: glycoprotein; lectin; macrophage; transmembrane protein
'Domain: transmembrane #status predicted <TRA>
16/Domain: C-type lectin homology <LCH>
1/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AEVQSLKTGLEA 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     )6 KAQ-LKSTSSLNSQIEVVNGKLKDSSRELQTLRRD---LSDVSALKSNVQMLQSNLQKAK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   )6 KAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSAAA 165
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es: 1-304 <SAT>
                                                                                                                                                                                                                                                 QSLDSRADSFEKGISSLKVDVEDHRQELQAGRDLSQKVTSLESTVEKREQALKTDLSDLT 143
                                                                                                                                                                                                                                                                                     LGIGILVLLIIVILGVPLIIFTIKANSEACRD--GLRAVMECRNVTHLLQQELTEAQKGF 81
                                                                                                                                                                                      QDVEAQAATCNHTVMALMASLDAEKAQGQ-----KKVEELEGEI----TTLNHKLQDAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----EMTSLKKDLETLTAQIQNANGHLEQTDTQIQGL 305
                                                                                                                                                                                                                                                                                                                                                                                33;
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A:Title: Periodic charge distributions in the myd R:Reference number: A93287; MUID:82272395
A:Accession: A93287
A:Molecule type: DNA
A:Residues: 847-1333, 'R',1335-1876, 'L',1878-1963
R:Wills, N.; Gesteland, R.F.; Karn, J.; Barnett, Cell 33, 575-583, 1983
                                                                                                                                                                                                                                                                                           A:Experimental source: clone F32A7
R;Karn, J.; Brenner, S.; Barnett, L.
Proc. Natl. Acad. Sci. U.S.A. 80, 4253-4257, 1983
A;Title: Protein structural domains in the Caenorhabditis ele
A;Reference number: A93958; MUID:83273600
A;Accession: A93958
A;Accession: A93958
A;Molecule type: DNA
A;Residues: 1-61,'EMSVIQ',65-376,'V',378-1963 <KAR>
A;Crosh-references: GB:J01050; NID:g156399; PIDN:AAA28124.1;
B;McTosh-Terences: GB:J01050; NID:g156399; PIDN:AAA28124.1;
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A; Reference number: A21074;
A; Accession: A21074
A; Molecule type: DNA
                                                                      A; Title: The genes sup-7 X and
                                                                                                                                                                                                                                                      R;McLachlan, A.D.; Karn,
Nature 299, 226-231, 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, A; Reference number: 219322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 13-Jun-1983 #sequence_revision 19-May-2000 #text_change 19-Jan-2001
C;Accession: T20770; T21629; A93958; A93287; A21074; A02992
R;Kershaw, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     myosin heavy chain B [similarity] - Caenorhabditis elegans N;Contains: myosin ATPase (EC 3.6.1.32) C;Species: Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 174, 4967-4976, 1992
A:Title: Architecture of the vir regulons of group A streptococci parallels opacity fact A:Reference number: A42711; MUID:92332431
A:Accession: A42711
A;Status: preliminary
A;Molecule type: DNA
A:Residues: 343-415 <HAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1963 <WIL>
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Molecule type: DNA
Residues: 1-1963 <WI2>
Cross references: EMBL 283107; PIDN:CAB05505.1;
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Accession: T21629
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Cross-references: EMBL; 281499; PIDN: CAB04089.1;
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MUID:83232892
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Pred. No. 2.2;
29; Mismatches
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RESULT

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A;Residues: 1-959 <BAR>
A;Cross-references: GB:U15589; NID:g558474; PIDN:AAC52151.1;
C;Keywords: membrane fusion; membrane trafficking
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F:1163-1963/Region: light meromyosin
F:125/Modified site: N6,N6.N6-trimethyllysine (Lys)
F:180/Binding site: ATP (Lys) #status predicted
F:702,712/Active site: Cys #status predicted
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change
C;Accession: A55913
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A; Cross-references: GB:V01494;
C; Genetics:
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Best Local :
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                                                              LLQ 180
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A;Residues: 1-376,'V',378-390,'V',392-576,'L',578-680,'I',682-1938 <DIB>
A;Residues: 1-376,'V',378-390,'V',392-576,'L',578-680,'I',682-1938 <DIB>
A;Cross-references: EMBL:X08065; NID:g6785; PIDN:CAA30854.1; PID:g6786
R:Karn, J.; Brenner, S.; Barnett, L.
Proc. Natl. Acad. Sci. U.S.A. 80, 4253-4257, 1983
A;Title: Protein structural domains in the Caenorhabditis elegans unc-54 myosin
A;Reference number: A93958; MUID:83273600
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A;Reference number: S02771; MUID:89178677
A;Accession: S02772
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R; Dibb, N.J.; Maruyama, I.N.; Krause, M.;
J. Mol. Biol. 205, 603-613, 1989
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A;Residues: 24-93,'E',95-97,'R',99-376,'V',378-388,'GDV',392-407,'N',409-473,'G',475-57
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A;Cross_references: EMBL;Z71261; PIDN:CAA95806.1; GSPDB:GN00019; CESP:R06C7.10
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:| | | | | | | | | | | | | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
      AAPQLLIV 171
                                                                                                                                GEGLVGSEELEELKRKQMNRVMDLQEALSAA-----QNKVISLEKAKGKLLAETEDARSD 1438
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Pred. No. 13;
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992
C;Accession: S07533
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S07533
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C; Date: 09-Jun-2000
В
                              Q
                                                                                                                                                              C; Keywords: coiled coil; glycoprotein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-286/Product: puff II/9A protein #status predicted <MAT>
F;156/Binding site: carbohydrate (Asn) (covalent) #status pro
                                                                                                                                                                                                                                                        A;Cross-references: GB:X51679; NID:g10113; PID:g1405812 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                   R;DiBartolomeis, S.M.; Gerbi, S.A.
J. Mol. Biol. 210, 531-540, 1989
A;Title Molecular characterization
A;Reference number: S07532; MUID:901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to GenBank, July 1995 A; Description: Isolation, seque
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A; Residues: 1-286 <DIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 puff II/9A-2 protein precursor - fungus gnat (Sciara coprophila)
C; Species: Sciara coprophila
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                                                                                                                                                                                                                                           A; Map position:
                                                                                                                                                                                                                                                                                                                                  A; Status: not compared with
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 68
                                46 IKANSEACRDGLRAVMEC-RNVTHL-----LQQELTEAQKGFQDVEAQAATCNHTVMAL 98
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LKREKEARQKAEKALKECQKNTENLKETTEQLKKELAEAQKALEKCKKELADCK--
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37; Conser
                                                                       th 10.9%; similarity 25.6%; 31; Conservative 2
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MUID:90133907
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4; Mismatches
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hypothetical protein M01A8.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C;Accession: S40998
R:Hawkins, T.; Thomas, K.
submitted to the EMBL Data Library, October 1993
A;Reference number: S40997
PAccession: S40998
Status: preliminary
Molecule type: DNA
A;Residues: 1-597 <HAWD
A;Cross-references: EMBL:227081
C;Genetics:
A(3, 754):13541-13641-23441-23441-23643-23643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-43643-4364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.9%; Score 96.5; DB 2; Length 597; Best Local Similarity 24.8%; Pred. No. 4.9; Matches 32; Conservative 29; Mismatches 39; Indels 2
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1: /cgn2_6/ptodata/2,

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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-055-094-4
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US-08-809-494A-4
US-08-809-494A-4
US-08-33-306A-4
US-08-33-306A-4
US-08-742-923A-4
US-08-742-923A-4
US-08-113-788-4
US-09-1113-788-4
US-09-1113-788-4
US-09-111-470-4
US-09-111-470-1
US-08-465-201-4
US-09-1164-2
US-08-465-746-2
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US-08-624-650-1
; Sequence 1, Application US/08624650
; Patent No. 5914252
; GENERAL INFORMATION:
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85	85	85.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	88	88	88	88	88
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Patent No. 5210183	Patent No. 5210183	Sequence 1, Appli	Sequence 9, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	<u>ა</u>	Sequence 4, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	23,	Sequence 23, Appl	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli

#### ALIGNMENTS

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Matches

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Query Match Best Local Similarity

100.0%; Score 889; DB 2; 100.0%; Pred. No. 4.3e-88;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -09-055-095-4
                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: Filed HUCLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                     TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                  Local
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                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc STREET: 3174 Porter Dr.
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                                                    Score 99.5; DB 2;
Pred. No. 0.0068;
5; Mismatches 41;
 ---ANITH--QEDILEGQ----
                                                                              Length 270;
                                                     Indels
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                                                                                                                                                                                      Matches
                                                                                                                                                                                                         Best Local
                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212 818-9479 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: GOLdberg, Jules E
REGISTRATION NUMBER: 2440
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
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     143 VLSVRIADKKYY--PSSQD 159
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                          83 DVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQ 142
                                                                                                              40 VLCLGLLVTVILLILQLSQVSDLIKKQQ----
                                                                                                                                                23 LLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQELTEAQKGFQ 82
                                                                                                                                                                                                                                                                                                                                       TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 7-
FILING DATE: 31-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/809,494A FILING DATE: 24-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 261 Ma
CITY: New York
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                                                                                                                                                                                     1 Similarity
36; Conserv
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                                                                                                                                                                                                                                                                                                                                  amino acid
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                                         ----ILAQRRSEKS-AQESQKELKEMIETLAHKLDEKSKKLMELHRQNL 124
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25.9%;
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                                                                                                                                                                                      25; Mismatches
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                                                                                                          ----- ANITH--QEDILEGQ---- 80
                                                                                                                                                                                                                         Length 270;
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125 NLQEVLKEAANYSGPCPQD 143

APPLICANT: Masaki, Tomoo

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US-09-352-302-2
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                                                                                    RESULT
              Sequence 4, Application US/08809494A Patent No. 5962260 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 6-3
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-2
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212 818-9479
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
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PRIOR APPLICATION NUMBER: JP 6-321705
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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 APPLICANT:
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                                                                                                                                      125 NLQEVIKEAANYSGPCPQD 143
                                                                                                                                                                      143 VLSVRIADKKYY -- PSSQD 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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Sawamura, Tatsuya
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                                                                                                                                                                                                                                                                                                                                                           11.2%; Score 99.5; DB 4
25.9%; Pred. No. 0.0068;
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US-09-352-302-4
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                                                                                                                                                                Sequence 4, Application US/09352302 Patent No. 6197937
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NÚMBER: 24408
REFERENCE/DOCKET NUMBER: JG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                              APPLICANT: Masaki, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION DATA:
PRIOR APPLICATION UMBER: JP
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CORRESPONDENCE ADDRESS:
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                                            CORRESPONDENCE ADDRESS
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                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                       143 VLSVRIADKKYY--PSSQD 159
                                                                                                                                                                                                                                                                     128 NLQEVLKEAANYSGPCPQD 146
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TELEPHONE: 212 818-9479
TD NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/809,494A FILING DATE: 24-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                            43 VLCLGLLVTVILLILQLSQVSDLIKKQQ-----ANITH--QEDILEGQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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              261 Madison Avenue
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                                                                                                                                 Sawamura, Tatsuya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                              McAulay Fisher Nissen Goldberg & Kiel
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                                                                                Modified Low-Density Lipoprotein Receptor
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Pred. No. 0
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Best Local Similarity
Trohes 36; Conserve
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                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08533306A Patent No. 5837457
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: JG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce,
STREET: P.O. Box 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7
FILING DATE: 31-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                            143 VLSVRIADKKYY -- PSSQD 159
                                                                                                                                                                                                                                                                                                                                                                                                            128 NLQEVLKEAANYSGPCPQD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 212 | 18-9479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                  COUNTRY:
                                                                                    STATE:
                                                                                                       CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 DVEAQAATCHHTVMALMASLDAEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQ 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 VLCLGLLVTVILLILQLSQVSDLIKKQQ------ANITH--QEDILEGQ----
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REGISTRATION NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
   COMPUTER:
                                                  ZIP: 48303
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                                                                                                    Bloomfield Hills
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Claxton, David
 E: Floppy disk
IBM PC compati
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compatible
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                                                                                                                                                                                      Markers for Detection of Chromosome 16 Rearrangements
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08742923A Patent No. 5869611
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Best Local (
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                                   TELEFAX: (810) 641-0270 INFORMATION FOR SEQ ID NO: 4:
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MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 366
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
                                                                                                 REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION: (810) 641-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA
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ATTORNEY/AGENT INFORMATION:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 TROKLNVSTKLROLEEERNSLODOLDEEMEAKONLERHISTLNIOLSDSK 324
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nes 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/742,923A FILING DATE: No. 5869611ember 1, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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SOFTWARE: PatentI
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PatentIn Release #1.0, Version #1.25
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                                                                                                                                    LNE....
DeAnn F.
NUMBER: 36683
NUMBER: 2115-00869DVC
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-742-923A-4

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; MOLECULE TYPE:
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Sequence 3, Application US/08938105
Patent No. 6353151
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Best Local Similarity
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                                                                                                                                                                        Matches
                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (303) 863-02 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1886 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
                                   1753 ALKGGKKQLQKLEARVRELENEL-----EAEQKRNAESVKGMRKSERRIKELTYQTEEDK 1807
                                                                                                   1693 AVQECRNAEEKAKKAITDAAMMAEELKKEQDTSAHLERMKKNMEQTIKDLQHRLDEAEQI 1752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
   161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 -AEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 CSDGERARAELNDKVHKLQNEVESVTGMLNEAEGKAIKLAKDVASLSSQLQDTQELLQEE 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPUTER KEADADDD COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERADRE: Patentin Release #1.0, Version
                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 CRDGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLD------
                                                                                                                                     59 AVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNH------TVMALMASLD-AEKA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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 SSAAAPQLLIVLLGL 175
                                                                  Q---GQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKY----YPSSQDS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
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1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vikstrom,
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                                                                                                                                                                        Conservative
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                                                                                                                                                                                      10.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.7%; Score 95; DB 2; 24.5%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/938,105
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                                                                                                                                                                                    Score 93.5; DB Pred. No. 0.46;
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RESULT 11
US-09-113-788-4
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Best Local :
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APPLICANT: Au-You
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                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 1235724
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LENGTH: 292 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                              144 NNNGEEASTE
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                                                                                           124 NHKLQDASAE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                     78 QKGFQDVEAQAATCNHTVMALMASLDAEKAQGQ-----
                                                                                                                                                                                   39 CHLLLSLGLGLLLI.VIICVVGF-----QNSKFQRDLVTLRTDFSNFTSNTVAEI---
                                                                                                                                                                                                               20 CKLL--LGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQELTEA 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                         ----QALTSQGSSLEETIASLKAEVEGFKQERQAVHSEMLLRVQQLVQDLKKLTCQVATL
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                                                                                                                                                                                                                                                             Similarity
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Goli, Surya K.
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linear
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                                                              153
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                                                                                                                                                                                                                                                           10.4%; 24.6%;
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                                                                                                                                                                                                                                                                        DB 2;
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Sequence 4, Applicati Patent No. 5969104 GENERAL INFORMATION:

Application US/09113788

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APPLICANT:

Au-Young, Janice

Cocks, Benjamin G

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US-09-111-470-4
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US-09-113-788-4
                                                                                                                                                Sequence 4, Application US/09111470 Patent No. 6277959
                                                                                                                                              Patent No.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
                                                                                               APPLICANT:
                               APPLICANT:
                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 1235724
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                             144 NNNGEEASTE
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                                                                                                                                                                                                                                                                                                          88 ----QALTSQGSSLEETIASLKAEVEGFKQERQAVHSEMLLRVQQLVQDLKKLTCQVATL 143
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                                                                                                                                                                                                                                                                                                                                                                                                      20 CKLL--LGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQELTEA 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
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 Lebecque, Serge J.E.
VENTION: Mammalian Membrane Protein Genes;
VENTION: Related Reagents
                                                                             Ravel, Odile
Bates, Elizabeth E.M
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                                                   Saeland, Sem
                                                                                                            Valladeau, Jenny
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                               Ford, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 92.5; DB:
Pred. No. 0.043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                       39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 292;
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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-310-187A-1
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Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/310,187A
CURRENT FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Benichou, Gilles
APPLICANT: Fedoseyeva, Eugenia
                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09310187A Patent No. 6358751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                           TITLE OF INVENTION: Involvement of Autoantigens in Cardiac TITLE OF INVENTION: Graft Rejection FILE REFERENCE: UCSF-090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (650)496-1200 INFORMATION FOR SEQ ID NO:
                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60
FILING DATE: 09-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin p.
REGISTRATION NUMBER: 34,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acid
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TELECOMMUNICATION INFORMATION:
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CITY: Palo Alto
STATE: Californi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 08-JUL-1998
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901 California Avenue
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                      Score 89.5;
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                                         DB 4;
       51;
                                         Length 1939;
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59 AVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNH-----TVMALMASLD-AEKA 107

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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: p
US-08-312-949-4
RESULT 15
US-08-446-201-4
; Sequence 4, Application US/08446201B
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: 30-SEP-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
address: Curtis, Morris & Safford, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Briles, David APPLICANT: Wu, Hong-Yin TITLE OF INVENTION: MUCC TITLE OF INVENTION: PNEU
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                                                                                                                              111 K-----KVEELEGEITTLNHKLQDA--SAEVERLRRENQVLSVRIADKK 152
                                                                                                                                                                  178 IAELENQVHRLEQELKEIDESESEDYAKEGFR------APLQSKLDAKKAKLS 224
                                                                                              225
                                                                                                                                                                                                    60 VMECRNVTHLLQQELTE------AQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2049
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                                                                                            KLEELSDKIDELDAEIAKLEDQLKAAEENNNVEDYFKEG--LEKTIAAKK 272
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Pred. No. 0.13;
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CURRENT FILING DATE: 1995-05-19
EARLIER APPLICATION NUMBER: 08/312,949
EARLIER FILING DATE: 1994-09-30
EARLIER FILING DATE: 1994-05-20
EARLIER APPLICATION NUMBER: 08/046,636
EARLIER APPLICATION NUMBER: 08/048,896
EARLIER FILING DATE: 1994-09-20
EARLIER FILING DATE: 1993-04-20
EARLIER FILING DATE: 1993-04-20
EARLIER FILING DATE: 1993-04-20
EARLIER APPLICATION NUMBER: 07/656,773
EARLIER APPLICATION NUMBER: 07/656,773
EARLIER FILING DATE: 1991-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6042838 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 4
LENGTH: 288
                                                                                                                                                                              Matches
                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BRILES, David E.
APPLICANT: WU, Hong-Yin
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR MUCOSAL ADMINISTRATION
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN A (PSPA)
FILE REFERENCE: 454312-2018
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                         111 K-----KVEELEGEITTLNHKLQDA--SAEVERLRRENQVLSVRIADKK 152
                                                                                        178 IAELENQVHRLEQELKEIDESESEDYAKEGER-----
                                                                                                                                60 VMECRNVTHLLQQELTE-----AQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQ 110
KLEELSDKIDELDAEIAKLEDQLKAAEENNNVEDYFKEG--LEKTIAAKK 272
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Search completed: June 4, 2002, 15:26:57 Job time: 130 sec

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Result
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n enhancing pre-B cell gresing it and useful in the Japanese.									sis; pre-B cell growth;	for enhancing pre-B cell			180 AA.	ALIGNMENTS	AAY22579 AAG67537	AAW00024	AAW54241	AAW02258	AAW98643	AAU01994	AAG67538	AAM79523	AAW59881	AAY31646 AAR53448	AAB93613	AAR99587	AAY24152 AAB85870	AAR99586	AAG64153	AAY33203 ·	AAY32768 AAY32764	AAY32766	AAY32763	AAW77292 AAW36951	AAG73947
growth - and he diagnosis of						,			enhancement.	growth.					Bacterial general Amino acid sequenc	മവ	Rattus norvegicus	Nucleolar/endosoma	H. pylori GHPO 363	ne #29 h		Human protein SEQ		Human transport-as	Human protein sequ	Low density lipopr	Bovine LDL recepto Bovine LOX-1 polyp	Canine ribosome re Low density lipopr	Polypeptide #2 for	Human HM1.24 antig	HM1.24 antigenic p	HM1.24 antigenic p	4 antigenic	Protein bound by A	olon cance

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Best Local Similarity
          The protein having the amino acid sequence below is bound specifically by a cytotoxic antibody which can be used in the treatment of lymphocytic tumours, including T-cell tumours and B-cell tumours other than myeloma. The antibody is preferably monoclonal and has ADCC or CDC type cytotoxicity. It may be chimeric or humanised, and preferably contains a human antibody constant region C gamma (such as C gamma 1 or C gamma 3). A preferred antibody is an anti-human HM1.24 antibody or an antibody which binds to an epitope recognising anti-human HM1.24 antibody. The cytotoxic antibody is useful in the treatment of lymphocytic tumours such as acute or chronic B lymphocytic leukaemia,
                                                                                                                                                                          Claim 1; Page 44-45; 82pp; Japanese.
                                                                                                                                                                                                                       Treatment of lymphocytic tumours using cytotoxic antibody - binding to specific antigen such as {\tt HM1.24} and effective against T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytotoxic antibody; anti-human HM1.24; lymphocytic pre-B lymphoma; Burkitt's lymphoma; T-cell tumour;
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pre-B
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Best Local S
Matches 180
                  A humanised anti-HM1.24 antibody has been developed which comprises human I and H chain C regions, and L and/or H chain V regions containing material originating in mouse anti-HM1.24 antibody. The V regions contain framework (FR) regions of human origin and complimentarity determining regions (CDR) of mouse origin, leading to a reshaped humanised antibody. The C regions are human Ck (L-chain) an human C gamma (especially C gamma 1) (H-chain). The FR regions of the L chain V region are derived from human subtype HSG1 (e.g. from human antibody RE1) and the FR regions of the H chain V region are derived from human antibody HG3 and FR4 from human subtype HSG1 (e.g. FR1-3 from human antibody HG3 and FR4 from human antibody JH6). The present sequence represents an antibody polypeptide from the present invention. The antibodies are used for the present invention.
polypeptide from the present invention. The antibodies are used the treatment of myeloma, especially by injection, intravenously, intramuscularly or subcutaneously. The antibodies are used at 0.0
                                                                                                                                                                                 Claim
                                                                                                                                                                                                       Humanised anti-HM1.24 antibody
                                                                                                                                                                                                                                 N-PSDB;
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                                            This invention describes a novel human antigenic protein, HM1.24, its encoding nucleic acid, splice variants and promoter region. The products of the invention have antirheumatic and antiarthritic activity. The DNA of the invention is isolated from bone marrow tumour cells, which can be used to study the expression of HM1.24 antigen, promoter activity of its promoter region, and in development of drugs in treating e.g. myeloma and rheumatoid arthritis. This sequence represents the human HM1.24 antigenic protein described in the invention.
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variants, useful e.g.
rheumatoid arthritis
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24-MAR-1998;
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DB; AAZ09726.
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98JP-0093883
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                                                                                                                                                                                                                                                                                                                                                   .24 antigen protein as well as splicing development of drugs for treating myeloma
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No. 6.2e-78;
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                                                                                                                                                                                     This sequence represents a human soluble HM1.24 antigenic protein. The invention relates to an immunochemical assay of anti-HM1.24 antibody by use of a soluble HM1.24 antigenic protein, or an immunochemical assay of the soluble antigen by use of the antibody. The immunoassay of the HM1.24 antigen or antibody is useful for diagnosis of immune disorders and cancer, for monitoring of anti-HM1.24 antibody immunotherapy, and for assay of the antibody or antigen for investigative purposes, in biological samples such as blood, serum, urine, milk, synovial fluid or microorganism culture media. The method is sensitive down to 500 pg/ml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoassay of anti-HM1.24 antibody or soluble HM1.24 antigen
useful for diagnosis of immune disorders and cancer
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                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                     Disclosure; Page 131-133;
                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-277273/23
N-PSDB; AAX59485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reconstituted human antibody; peptide antigen HM1.24; framework region; complementary determining region; CDR; anti-HM1.24 antibody; myeloma; humanised antibody.
                                                                                                                                                                                                                                                                                                                                       Reconstituted human antibody useful in the treatment of myeloma
                                                                                                                                                                                                                                                                                                                                                                                              Tsuchiya
                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            multiple myelomas which are resistant to conventional treatment, acute B-lymphocytoma, chronic B-lymphocytoma, pre-B lymphoma, Bulymphoma, acute T-lymphocytoma, chronic T-lymphocytoma, and PNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for the treatment of lymphoma, in whic a cytotoxic antibody is potentiated by administration of a biological response modifier. The method can be used for treatment of lymphomas and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody potentiator; lymphoid tumour; lymphoma; cytotoxic antibody; multiple myeloma; acute B-lymphocytoma; chronic B-lymphocytoma; pre-B lymphoma; Burkitt's lymphoma; acute T-lymphocytoma; therapy; chronic T-lymphocytoma; PNTL.
                          AAY07250 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-AUG-1998;
14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 37-38; 62pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potentiation of antibody treatment of lymphoma response modifier % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX36561.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-1999
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Local Similarity 100.0%;
nes 180; Conservative 0
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97JP-0280759
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                       Protein; 180
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Pred. No. 6.2e-78;
Mismatches 0;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the mouse BST-2 protein which is used to raise antibodies, especially the monoclonal antibody RS38. The antibody can lused in compositions to treat myelomas when the antibody is associated with a cytotoxic activity.
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                                                                    WO200017395-A1
                                                                                                                                                            multiple
                                                                                                                                                                                                                                                 Human HM1.24 antigen protein
                                                                                                                                                                                                                                                                                              21-JUL-2000
                                                                                                                                                                                                                                                                                                                                              AAY53273;
                                                                                                                                                                                                                                                                                                                                                                                        AAY53273 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An agent for treating myeloma -includes an antibody and cytotoxic activity % \left( 1\right) =\left\{ 1\right\} 
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                                                                                                                                                                                                         Human;
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                                                                                                                                                                               HM1.24 antigen protein; detection; plasmocytoma; le myeloma; plasmocytic leukaemia; extramedullary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BST-2; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX29996
                                                                                                                                                         plasmocytoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 AA;
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Pred. No. 6.2e-78;
; Mismatches 0;
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                                                                                                                                                            myeloma.
                                                                                                                                                                                 extramedullary plasmocytoma;
                                                                                                                                                                                                                                                    NO:2.
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Best Local Sin
Matches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in plasmocytomas before quantifying the amplification product by comparing with results obtained with a control sample. The method is for detecting or measuring plasmocytomas, applicable for early diagnosis of e.g. multiple myeloma, plasmocytic leukaemia, isolated plasmocytoma, extramedullary plasmocytoma, multiple plasmocytoma obtained from smoking or asymptomatic myeloma. The present sequence represents human HM1.24 antigen protein, which is expressed in plasmocytomas and so can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A method has been developed for detecting or measuring plasmocytomas in a sample at an early stage of disease development. The method comprises amplifying a polynucleotide which is expressed specifically or strongly
                                                      mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma undifferentiated carcinoma; clear call adenocarcinoma; cystadenofibroma; adenofibroma; sernial analysis of gene expression; SAGE; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic;
                                                                                                                                             Ovarian tumour marker gene; human; overexpression; upregulatie epithelial tumour; cancer; diagnosis; prognosis; disease monitientification; serous cystadenoma; borderline serous tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection or measurement of plasmocytomas, applicable for early diagnosis of e.g. multiple myeloma and plasmocytic leukemia, us polynucleotide which is expressed specifically or strongly in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 15-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHUS
                                                                                                                                   serous cystadenocarcinoma; mucinous cystadenocarcinoma;
                                                                                                                                                                                                               Bone marrow stromal antigen
                                                                                                                                                                                                                                               08-FEB-2002
                                                                                                                                                                                                                                                                                                         ABB50295 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the method of the invention.
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                                                                                                                                                                                                                                                                                                           Protein;
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                                                                                                                                                                                                                (BST-2) ovarian tumour marker
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Pred. No. 6.2e-78;
Wismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Japanese.
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                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                n; upregulation; disease monitor
                                                                                                                      endometrioid carcinoma
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                                                                                                                                                                monitoring;
                                                                                                                                                                                                               protein,
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 889; DB 22; Best Local Similarity 100.0%; Pred. No. 6.2e-78; Matches 180; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA83181-ABA83122, ABA83180, ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179, ABA83181 and ABA83183). The methods of the invention are useful for detecting an ovarian tumour in a pattent, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for assessing the relative severity of ovarian cancer, in tests for assessing the relative severity of ovarian cancer and in tests for monitoring a patient in remission from ovarian cancer and in tests for monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an epithelial ovarian tumour selected from serious cystadenoma, borderline serious tumour, serious cystadenocarcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mucinous cystadenoma, borderline mucinous tumour, mucinous cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner tumour. The ovarian tumour marker genes of the invention were identified using SAGE (serial analysis of gene expression) and were found to be overexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovarian epithelial cells. The marker genes are implicated in immune response pathways, in the regulation of cell proliferation and in protein folding, and many of these are membrane-localised or secreted. In addition to their use as diagnostic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting and identifying ovarian tumor, identifying increased risk developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor max
                       AAB70697 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and prevention of ovarian cancer. Sequences ABB50257 ABB50299 represent proteins encoded by ovarian tumour marker genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-2000; 2000US-194336P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                       TTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSAAAPQLLIVLLGLSALLQ 180
                                                                                                                                                                                                                                                                    MECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEI 120
                                                                                                                                                                                                                      \verb|mecrnvthllqqelteaqkgfqdveaqaatcnhtvmalmasldaekaqgqkkveelegei|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-626450/72
)B; ABA83121.
                                                                                                                                   ttlnhklqdasaever1rrenqv1svriadkkyypssqdsssaaapq11iv11g1sal1q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                             Page 124; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sherman-Baust CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 AA;
                       Protein;
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                         8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; HM1.24 antigen expression potentiator; HM1.24 protein antigen;
myeloma; interferon alpha; interferon gamma; IFN-alpha; IFN-gamma;
interferon regulatory factor 2; IRF-2; cytostatic; cytotoxic antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\rm HM1.24} antigen expression potentiating agent containing alpha or gamma or IRF-2 for treatment of myeloma -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-202921/20
N-PSDB; AAF74792.
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16-FEB-2000; 2000JP-0038689
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 55-56; 72pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kosaka M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-2000; 2000WO-JP05617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multiple myeloma
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121 TTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSAAAPQLLIVLLGLSALLQ
                                                                                                                                                                                                                                                                                                                       Local Similarity nes 180; Conserv
                                                                                                         61
                                                                                                                                                           61
                                                                                                                                                                                                             mecrnvthllqqelteaqkgfqdveaqaatcnhtvmalmasldaekaqgqkkveelegei
                                                                                                                               MECRNYTHLLQQELTEAQKGFQDYEAQAATCNHTYMALMASLDAEKAQGQKKYEELEGEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ozaki S,
                                                                                                                                                                                                                                                                                                                    100.0%; Score 889; DB 22; ilarity 100.0%; Pred. No. 6.2e-78; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ
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Best Local Similarity
                                                                                                                                                                                                                                                     present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present sport of No:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                and
and
                                                                                                                                                                                                                                                                                                                                                                    expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell by inserting the nucleic acids into a host cell and culturing the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the preventic diagnosis and treatment of diseases associated with inappropriate P
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                             to express the proteins. N and P can be used in the prevention, and treatment of colorectal carcinomas and cancers. AAH37196 to and AAB77789 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the proteins are collectively known as colon cancer antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer-associated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 6512-6513; 9803pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding 4277 human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
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03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human;
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              TTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSAAAPQLLIVLLGLSALLQ 180
                                                                                                           MECRNYTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEI 120
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ttlnhklqdasaeverlrrenqvlsvriadkkyypssqdsssaaapqllivllglsallq
                                                       mecrnvthllqqelteaqkqfqdveaqaatcnhtvmalmasldaekaqgqkkveelegei
                                                                                                                                                                      180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for preventing,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH33378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carcinoma;
                                                                                                                                                                                                                                           193
                                                                                                                                                                     100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
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99US-0163280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               colon cancer antigen; diagnosis;
; chromosome 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosing
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                                                                                                                                                                   Score 889; DB 22;
Pred. No. 6.8e-78;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      colon cancer-associated polypeptides,
and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
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the
                                                                                                                                                                   Gaps
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193
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RESULT

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Human; secreted protein; molecular weight marker; genetic fingerprinting; antibody production; nutritional supplement; therapy; clone 0238\_1;

Protein encoded by clone 0238\_1.

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RESULT 14
AAW36951
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XXXX DXX AXX
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Best Local S
Matches 179
                                                                                                                                                                                                                                                                                                                                                      The Anti-HMI.24 antibody can be used in the production of lymphocyte activation inhibitors. These inhibitors can be used for the prevention and treatment of autoimmune diseases, rejection reactions in organ transplant or allergy. Administration is non-oral, e.g. by intravenous and intramuscular injection, local or systemic.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Lymphocyte activation inhibitor comprises antibodies, particularly anti-HM1.24 antibody - for preventing and treating auto:immune diseases, rejection reactions in organ transplant or allergy
                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 38-39; 53pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-480937/41.
N-PSDB; AAV59114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-HM1.24; antibody; lymphocyte activation inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein bound
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                                                   12-MAY-1998
                                                                        AAW36951;
                                                                                             AAW36951 standard;
                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                  MECRNYTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
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                                                                                                                                               \verb|ttlnhklq| dasae verlrrenq vlsvriadkkyyps sqdsssaaapqllivllg lsallq|
                                                                                                                                                            TTLNKKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSAAAPQLLIVLLGLSALLQ
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99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is a protein encoded by clone 0238_1, which is a polynucleotide of the invention. The DNA encoding this sequence was isolated from a human dendritic cell cDNA library. The polynucleotide, which encodes a secreted protein, can be used, e.g. as a tissue or molecular weight marker, in genetic fingerprinting, to raise anti-protein or anti-DNA antibodies and in interaction trap assays. The protein can be used to assay biological activity raise antibodies for use in used to assay biological activity raise antibodies for use in the anti-interaction and as a nutritional supplement. It may also have a very wide range of therapeutic and biological activities (no examples are given to support. this), e.g. cytokine or modulator of cell proliferation and differentiation, immunostimulant or immunosuppressant, haematopoiesis regulator, bone, cartilage, tendon, ligament and/or nerve tissue growth stimulator, bone, cartilage, tendon, ligament and/or nerve tissue growth biorhythm, metabolism or behaviour modifier, anti-depressant or analgesic or regulator. The transation of the process of
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Best Local Similarity
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Spaulding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-APR-1997;
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DB; AAV00426.
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Pred. No. 1.7e-73;
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N-PSDB; AAZ10915.
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                     DSSSAAAPQLLIVLLGLSALLQ 180
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immunotherapy monitoring.
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95.1%;
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